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(54) Title: IMMUNOGENIC CEA

(57) Abstract: The present invention provides for methods for immunizing actively against autologous carcinoembryonic antigen
(CEA). The method encompasses that the immune system is engaged with variant CEA which is either administered as a protein
vaccine, or is effected expressed by nucleic acid vaccination or live/viral vaccination. Preferred embodiments include immunization
with variants that include at least one foreign T-helper epitope introduced in the CEA sequence. Also disclosed is variant proteins,
DNA, vectors, and host cells useful for practising the method of the invention.

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IMMUNOGENIC CEA

FIELD OF THE INVENTION

The present invention relates to therapeutic vaccination ("active therapeutic immunotherapy") against diseases characterized by cells that express carcinoembryonic antigen, CEA. In particular, the present invention relates to the field of cancer therapy and cancer amelioration, where the cancer is characterized by cells that express CEA.

BACKGROUND OF THE INVENTION

Vaccination has become standard procedure for the prevention of numerous infectious diseases. The application of vaccines to other diseases, such as cancer, is now possible owing to advances in molecular engineering and a better understanding of tumour immunology. The concept of vaccines for cancer treatment is not new and was suggested nearly 100 years ago. Over the years, many attempts have been made to generate effective cancer "vaccines" from mixtures of tumour cells and infectious particles (so-called Coley's toxins) without much success. During this time, studies of transplantable tumours in animals established the feasibility of tumour rejection through immune-mediated mechanisms. These studies suggested that tumour cells expressed unique antigens (i.e. antigens that were not found on normal cells). These antigens, under appropriate conditions, could be recognised by components of the immune system. Further research identified many of the antigens that induced tumour rejection as normal self-proteins. There are many reasons why self-proteins might be recognised

by the immune system, including the presence of mutations in the coding regions of the protein, unusually high expression levels of the protein, and abnormal glycosylation of the protein. The awareness that T lymphocytes (T cells) are signifi-
5 cant mediators of tumour rejection has focused attention on the isolation of antigens that are specifically recognised by T cells. T cells recognise antigens as smaller fragments of proteins, so-called T cell epitopes, only after their intra-cellular degradation and presentation on the cell surface,
10 where they are bound to the major histocompatibility complex. The first T-cell-specific tumour antigen was derived from ma-lignant melanoma cells; subsequently, many other tumour anti-gens in a variety of tumours have been found to possess T-cell-specific epitopes.

15 CEA was one of the first tumour-associated antigens to be identified and has been well characterised. CEA is an oncofe-tal glycoprotein, which is found at high levels in the fetal colon and at lower levels in the normal adult colonic epithe-lium. CEA occurs at abnormally high levels in several benign
20 disorders and in some malignant tumours, including those of the stomach, small intestine, colon, rectum, pancreas, liver, breast, ovary, cervix and lung. Recently, several T-cell epi-topes within CEA that are recognised by human T cells have been described. Several different strategies are now using
25 vaccination to target CEA, and clinical trials have started to yield interesting findings.

Successful vaccination against CEA could affect many individu-als who have cancer and even more individuals who are at risk of developing cancer. Thus far, CEA appears to be a promising
30 antigen for vaccine therapy.

Biology of CEA: CEA is a 180-kD glycoprotein that is present
at high levels in colon epithelial cells during embryonic de-
velopment. Levels of CEA are significantly lower in colon tis-
sue of adults, but can become elevated when inflammation or
5 tumours arise in any endodermal tissue, including that in the
gastrointestinal tract, respiratory tract, pancreas and
breast. CEA was originally isolated from a colon carcinoma
specimen in 1965. The construction of monoclonal antibodies
against CEA has allowed the detection of the overexpression of
10 CEA protein in a variety of adenocarcinomas, including gas-
tric, pancreatic, small intestine, colon, rectal, ovarian,
breast, cervical and non-small-cell lung cancers. Currently,
~500 000 individuals are diagnosed with CEA-producing tumours
each year in the USA alone. Epithelial cells in several non-
15 malignant disorders, including diverticulitis, pancreatitis,
inflammatory bowel disease, cirrhosis, hepatitis, bronchitis
and renal failure and also in individuals who smoke also ex-
press CEA. This fact has made it difficult to use serum CEA
determination as a sensitive method for cancer screening. How-
20 ever, serum CEA levels have been useful in monitoring indi-
viduals for the recurrence of cancer.

In 1986, the gene that encodes human CEA was localised to
chromosome 19, and subsequently cloned (Okinawa S. et al.
1987, Biochem. Biophys. Res. Commun. 142, 511-518). In humans,
25 the CEA gene encodes a messenger RNA (mRNA) that is 3100 base
pairs long and translates to a protein that has a molecular
weight of 70 kD. The additional weight of the protein is pro-
vided by an extensive pattern of carbohydrates that are added
by glycosylation enzymes, leading to a final weight of 180 kD.
30 The structure of CEA protein includes an N-terminal sequence
followed by three disulphide-linked repeats of 178 amino a-
cids, and a hydrophobic C-terminal. This structure is similar

to that of the immunoglobulins, and has established CEA as a
member of the superfamily of immunoglobulin genes. A unique
feature of CEA is that it is linked via lipid into the mem-
brane, through a glycosylphosphatidylinositol moiety, making
5 it distinct from other members of the CEA. Several other anti-
gens are closely related to CEA, including the non-specific
cross-reacting antigen (NCA), biliary-specific glycoprotein
(BGP), CEA gene family member CGM-6 and pregnancy-specific
glycoproteins. Some of these represent separate species,
10 whereas others may be splice variants of CEA. Currently, 29
separate genes have been identified as coding a CEA-related
gene product, and most of these genes are located on the long
arm of chromosome 19.

The function of CEA in normal colon epithelial cells and in
15 tumour cells is not entirely clear. Many members of the immu-
noglobulin gene family serve as recognition markers, and this
might be true for CEA as well. Studies have reported that CEA
localised on the cell surface of colon tumours and other cells
can act as a homotypic adhesion molecule, resulting in the ag-
20 gregation of CEA-expressing cells. Furthermore, although CEA
is produced at low levels in normal colonic epithelial cells
in adults, the pattern of localisation differs from that ob-
served in most colon tumour cells or in the developing embry-
onic colon. In normal colonocytes, CEA is localised only at
25 the luminal surface of the cells, whereas in tumour cells, it
is found in a disordered pattern throughout the cell membrane.
Thus, current models suggest that CEA promotes the spatial
orientation of colon epithelial cells to one another and to
the surrounding matrix during embryonic development of the co-
30 lon, and helps maintain the integrity of the luminal epithe-
lium in the adult colon. The altered pattern of localisation
in tumour cells may help to disrupt the intercellular adhesion

of colonocytes, resulting in the disorganised growth and move-
ment of malignant cells. CEA may also be involved in the en-
hancement of metastatic disease. Elevated levels of CEA in the
serum have been shown to correlate with an increased incidence
5   of liver metastases, and this may be due to adhesion between
circulating CEA in the liver and CEA bound to metastatic tu-
mour cells. This may explain the high incidence of hepatic me-
tastases in those patients who have primary tumours that ex-
press CEA.

10 Several different lines of investigation have suggested the
possibility that CEA can serve as an antigenic target for
eliciting anti-cancer immune responses. Adaptive immune re-
sponses to any antigen can be broadly characterised by the
production of specific antibodies (i.e. humoral immunity) or
15 the generation of antigen-specific T cells (i.e. cellular im-
munity). Shortly after the discovery of CEA protein, several
groups sought to determine whether individuals who had colon
cancer developed anti-CEA antibodies during the course of
their disease (Ura Y et al. 1985, Cancer Lett. **25**, 283-295;
20 Frenoy N et al. 1987, Anticancer Res **7**, 1229-1233). Some
groups did not find significantly elevated titres of such an-
tibodies; however, others did find evidence that antibody re-
sponses to CEA occurred in some individuals. The potential for
CEA to elicit T-cell responses was first suggested by the ob-
25 servation that individuals who had colon cancer often exhi-
bited a delayed-type hypersensitivity (DTH) response to puri-
fied CEA protein (Orefice S et al. 1982, Tumori **68**, 473-475).
More recently, recombinant vaccinia virus expressing CEA were
administered to cancer patients, and CEA-specific T cells were
30 subsequently cloned from these patients, demonstrating that T
cells can recognise CEA (Tsang KY et al. 1995, J Natl Cancer
Inst **87**, 982-990). Several independent groups have now re-

ported the existence of multiple epitopes within CEA that are
recognised by human T cells that bind to various HLA class I
molecules (Tsang KY *et al.* 1995, J Natl Cancer Inst 87, 982-
990; Kawashima I *et al.* 1999, Cancer Res **59**, 431-435; Nukaya I
5 *et al.* 1999, Int J Cancer **80**, 92-97).

Prior srategies for CEA cancer vaccine development: Two lines
of evidence have supported the use of CEA as a target for vac-
cine development: the high level of expression of the CEA gene
in many different human tumours, and the emerging information
10 about the molecular biology and immunology of CEA. The experi-
mental generation of monoclonal antibodies against CEA paved
the way for a variety of diagnostic and therapeutic approaches
for cancer therapy based on the detection and targeting of
CEA. These have included the direct, *in vivo* use of anti-CEA
15 monoclonal antibodies, either alone or coupled to radioiso-
topes or cellular toxins, and also the use of anti-idiotype
antibodies. Strategies that target CEA-reactive T cells have
also been proposed, including the use of specific HLA-re-
stricted peptides derived from CEA, recombinant viruses and
20 bacteria expressing CEA peptides or proteins, and the pulsing
of CEA into antigen-presenting cells (APCs). Dendritic cells
are the most potent type of APC. Thus, dendritic cells loaded
with CEA peptides, DNA or RNA have been used to stimulate T
cells (Nair SK *et al.* 1999, Int J Cancer **82**, 121-124).

25 **Monoclonal-antibody therapy:** Monoclonal antibodies directed
against CEA were initially used for diagnostic purposes, in-
cluding the immunohistochemical staining of tissue specimens
and the localisation of disease in vivo. The use of antibody-
targeted therapeutics for cancer treatment has shown that tu-
30 mour-cell lysis can be initiated by immune-mediated mecha-
nisms. Antibodies can also be used for the direct delivery of

cytotoxic molecules such as radionuclides, toxins or chemo-
therapy agents to the site of an established tumour.

The discovery that anti-CEA antibodies can be used to detect
CEA-expressing tumour cells hinted that they could also be
5 used to mediate the rejection of tumour cells through immune
mechanisms. When anti-CEA antibodies bind to the surface of a
tumour cell, several pathways are activated, which can result
in the destruction of an antibody-marked cell. The presence of
bound antibody can activate the complement cascade, leading to
10 cell lysis (complement-mediated cytotoxicity). Another pathway
that might be more relevant to tumour cells is the initiation
of antibody-directed cellular cytotoxicity (ADCC). This cyto-
toxic reaction occurs when the Fc portion of an antibody binds
to and triggers Fc-receptor-bearing natural killer cells to
15 release cytotoxic granules that lyse cells that are coated
with the antibody. However, these anti-tumour effects depend
on the presence of CEA on the surface of targeted tumour
cells, and because CEA is often found in a heterogeneous pat-
tern, it is difficult to eradicate all of the cells within a
20 tumour mass. Furthermore, the anti-CEA antibody must be able
to circulate throughout the body and penetrate solid tumours.
This often cannot occur owing to an inadequate blood supply to
the tumour. Because many of the monoclonal antibodies that are
developed for *in vivo* clinical use are derived from mice,
25 strong human anti-mouse antibodies (HAMA) can be induced in
the patient upon repeated use of the monoclonal antibody;
thus, the mouse monoclonal antibody is eliminated before it
reaches the tumour.

Using another approach, anti-idiotype antibodies can be used
30 to either elicit or amplify an antigen-specific immune re-
sponse. For example, immunisation with CEA protein induces the

production of Ab1 antibodies. The antigen-binding site of an Ab1 antibody contains a hypervariable complementarity-determining region, which is complementary to the epitope on the antigen that is bound by the antibody. This region is also
5 known as the idiotype, and can induce the production of host antibodies. Immunisation with these idiotypes generates a series of anti-idiotype antibodies, known as Ab2 antibodies, which can resemble some of the epitopes of the original antigen. Thus, Ab2 antibodies then induce the production of anti-
10 anti-idiotype antibodies (Ab3 antibodies), which can specifically bind to the original antigen. The experimental *in vivo* use of an Ab2 antibody generated against CEA protein in mice has been described; Ab2-immunised mice were protected against challenge with lethal doses of CEA-expressing tumours (Pervin
15 S *et al.* 1997, Cancer Res **57**, 728-734). Clinical trials of this antibody have been conducted, and most patients did develop Ab3 responses that were specific for CEA (Foon KA *et al.* 1995, J Clin Invest **96**, 334-342). Furthermore, one of four patients tested also developed T-cell responses to CEA, although
20 no objective clinical responses were observed (Foon KA *et al.* 1997, Clin Cancer Res **3**, 1267-1276).

Another method of using monoclonal antibodies for cancer therapy is to conjugate them to a radionuclide, which can deliver damaging radiation to the vicinity of the tumour. The advan-
25 tage of this approach is that targeting a single cell expressing CEA can also lead to the death of nearby tumour cells that are not expressing CEA, owing to a by-stander effect. A similar approach can be used to deliver chemotherapeutic drugs that are known to be toxic to the tumour cells. This is accom-
30 plished by conjugating the chemotherapeutic drug to the anti-CEA antibody. The administration of the conjugated antibody results in the accumulation of toxic drug at the site of the

tumour rather than in normal tissues. Yet another approach is the construction of genetically modified monoclonal antibodies that are fused with cellular toxins, such as ricin. All of these specialised antibodies can have a by-stander effect,

5 avoiding the problem of heterogeneous CEA expression, but because of the size of the antibody conjugates, delivery and HAMA responses are still problematic. The use of humanised monoclonal antibodies, or chimaeric antibodies that contain only the murine variable regions that interact with antigen

10 combined with human Fc portions, seems to avoid or reduce the HAMA response. However, the delivery of such antibodies to the tumour site still remains a problem. The variable region of the antibody is used to target the cells, and is contained within the Fab portion of the antibody molecule. Because only

15 the Fab fragment is necessary for antigen recognition, smaller antibody fragments containing the Fab protein can be used for targeting tumour cells and enhancing delivery to sites of tumour growth.

CEA-derived peptides: T cells appear to play a major role in

20 tumour rejection after vaccination. Antibodies recognise their antigens by the three-dimensional structure of a single antigenic determinant, the so-called epitope. However, T cells recognise antigen only after the antigen has been processed into smaller linear peptide fragments, which are also known as

25 T cell epitopes. These epitopes are loaded onto specific molecules called major histocompatibility complex (MHC) proteins, so called because they are known to mediate transplantation rejection. MHC class I molecules are found on all nucleated cells, and are recognised by the T-cell receptors (TCRs) of

30 CD8+ T cells. MHC class II molecules are mainly expressed by APCs, and are recognised by CD4+ T cells. As will appear from the present specification and claims, especially peptides

binding to MHC Class I molecules would be of interest since
these are necessary in order to stimulate a CTL response
against a CEA bearing tumour cell.

Several experimental approaches have been used to identify CEA
5   epitopes that are presented by MHC class I molecules to CD8+ T
cells. Thus far, the most commonly used approach has been the
identification of a putative peptide sequence by using a com-
puter to predict binding affinity to specific MHC class I
molecules. This is now easy because the amino acid sequence of
10   the CEA protein has been determined and all nine potential
amino acid sequences can be quickly modelled. The peptide
groove of an MHC class I molecule normally binds short peptide
fragments that comprise 8-10 amino acids, and because the
three-dimensional structure of several MHC molecules is known,
15   the computer models can predict the potential peptides that
would be expected to bind with high affinity (Rammensee HG et
al. 1995, Immunogenetics **41**, 178-228). These peptides can be
synthesised and tested in vitro for their actual binding af-
finity for the MHC molecule and for recognition by specific
20   CTLs (Celis E et al. 1994, PNAS USA **91**, 2105-2109; Hill AV et
al. 1992, Nature **360**, 434-439; Houbiers JG et al. 1993, Eur J
Immunol **23**, 2072-2077).

The above-described method was used to isolate the first HLA-
restricted CEA peptide, namely carcinoembryonic-antigen-asso-
25   ciated peptide 1 (CAP-1). CAP-1 peptide binds to the HLA-A2
complex, and has been used to generate T-cell lines (i.e. a
mixed T-cell population that responds to CEA) from cancer pa-
tients who have been vaccinated with recombinant vaccinia vi-
rus expressing CEA. A T-cell clone (i.e. a single, genetically
30   identical T-cell population that recognises CEA) derived from
one of these patients has been shown to lyse target cells that

contain CAP-1 and the HLA-A2 complex. To date, several CEA
peptides that specifically bind to known HLA molecules have
been identified and have elicited T-cell responses. These pep-
tides can be used to immunise individuals who express the same
5 HLA molecule if these individuals do not tolerate the epitope.

Modified CEA peptides: CEA is a self-antigen and is generally
considered to be weakly immunogenic if not non-immunogenic.
The main reason for this is that CEA does not include T_H epi-
topes that can induce CD4+ cells to provide the necessary
10 helper functions to B lymphocytes and CTLs.

One method for enhancing recognition is to alter the affinity
of a CEA peptide for MHC molecules or T-cell receptors by
amino acid substitutions of peptide anchor residues or non-an-
chor residues, respectively. This strategy can be applied to
15 any known peptide epitope and might increase the immunogeni-
city of self-antigens. Modifications in the anchor binding
residues have resulted in higher affinity binding and better
T-cell responses for several melanoma antigens. The CEA pep-
tide CAP-1 was modified by replacing an asparagine residue (N)
20 with an aspartic acid residue (D) at position 6 (Zaremba S *et
al.* 1997, Cancer Res **57**, 4570-4577). The resulting "agonist"
peptide, designated CAP-1-6D, was recognised by T cells more
efficiently than the native CAP-1. Although modified peptides
can be used as therapeutic vaccines, the CAP-1-6D peptide has
25 yet to be tested in clinical trials.

Recombinant CEA protein: MHC-class-I-restricted CEA peptides
have, as mentioned above, been identified and have been shown
to generate CEA-specific T-cell responses; however, such pep-
tides can be used in a clinical setting to treat only those
30 patients whose MHC type is analogous to that of the peptide.

Additionally, effective anti-tumour immune responses might de-
pend on the presentation of multiple CEA epitopes through all
available MHC molecules expressed in each individual. This in-
crease in peptide diversity can be accomplished by delivering
5   the full-length protein to APCs. Sources of CEA protein in-
clude preparations from either tumour biopsy specimens and/or
supernatants derived from tumour-cell lines, both of which can
contain contaminants. Studies have shown that better humoral
and cellular immune responses were elicited in mice by priming
10   (i.e. administering a first vaccination) with recombinant vac-
cinia virus containing CEA followed by boosting (i.e. admini-
stering a second vaccination) with recombinant CEA protein
than by vaccination with either virus or protein alone (Bei R
et al. 1994, J Immunother Emphasis Tumor Immunol 16, 275-282).
15   Also baculovirus systems have been examined. Intramuscular in-
jection of recombinant baculovirus containing human CEA pro-
tein has been evaluated in a clinical trial involving five in-
dividuals who had metastatic breast cancer that responded to
hormonal therapy. Two of the patients produced both lymphopro-
20   liferative responses (i.e. T-cell stimulation and growth) to
recombinant CEA protein and strong DTH responses (as revealed
by a skin test) after immunisation (Conry RM et al. 1995, J.
Immunother. 18, 137). In another clinical trial, patients who
had colorectal carcinoma were immunised using either recombi-
25   nant baculovirus containing human CEA alone or in combination
with the cytokine granulocyte-macrophage colony-stimulating
factor (GM-CSF). All six of the patients who received the com-
bination treatment showed early CEA-specific T-cell prolifera-
tion after immunisation, whereas only two of the six patients
30   who were immunised with recombinant baculovirus containing CEA
without GM-CSF developed an anti-CEA T-cell response after
multiple vaccinations (Fagerberg J et al. 1995, J. Immunother.
18, 132). These studies provide good evidence for the use of

recombinant CEA protein as a boost following primary viral im-
munisation, or for its use in combination with immune-stimula-
tory cytokines.

DNA vaccines: DNA vaccines consist of a bacterial plasmid that
5 contains genes (e.g. pathogens, allergens or tumour antigens)
that are under the control of a strong eukaryotic promoter.
The DNA is usually taken up into host cells, where the encoded
antigen is produced and processed via both MHC class I and II
pathways, inducing CD8+ and CD4+ T-cell responses. In contrast
10 to viral vaccines, DNA vaccines are relatively simple to pro-
duce; moreover, they do not inhibit the immunological respon-
ses (e.g. downregulate the MHC class I pathway) that are often
associated with viral infections. Naked DNA (i.e. plasmid DNA
in saline) has been used for vaccination; this resulted in
15 stable expression after intramuscular injection and the induc-
tion of both cellular and humoral (antibody) immune responses.
The immune mechanisms involved are only partly understood. It
has been suggested that nucleic acid might be taken up selec-
tively by macrophages and/or APCs in the muscle. These acti-
20 vated macrophages then migrate to draining lymph nodes, where
they stimulate naive T cells.

A plasmid that encoded the full-length human CEA has been
tested by injecting it intramuscularly into mice; both CEA-
specific humoral and cell-mediated immune responses were in-
25 duced. This DNA vaccine also protected mice from a challenge
with CEA-expressing colon tumours (Conry RM *et al.* 1994, Can-
cer Res **54**, 1164-1168).

Dendritic cells: Dendritic cells are the most potent APCs and
present antigen via the MHC class I and MHC class II pathways.
30 The use of dendritic cells that have been pulsed (i.e. exposed

for a short time to high concentrations) with specific anti-
gens has been proposed as a means of generating more-effective
antigen-specific T-cell responses against CEA. In a Phase I
study, patients who had advanced malignancies expressing CEA
5 were vaccinated with dendritic cells that had been pulsed with
the CEA peptide CAP-1. A minor clinical response was observed
for one of the patients in the study, and disease progression
was stabilised in another (i.e. there was no tumour growth
following vaccination). No treatment-related toxicities were
10 observed, ting the feasibility and safety of this treatment
method (Morse MA et al. 1999, Clin Cancer Res 5, 1331-1338).
Dendritic cells that had been pulsed with a cocktail of mela-
noma peptides or a tumour lysate were used to treat patients
who had advanced melanoma by injecting the cells into or near
15 lymph nodes. Five patients out of 16 produced a clinical re-
sponse to the vaccine, and two of the five responded com-
pletely (Nestle FO et al. 1998, Nat Med 4, 328-332).

Another approach used CEA-specific mRNA and total RNA derived
from CEA-expressing tumour cells. RNA encodes multiple CEA
20 epitopes for various HLA types meaning that patients can be
immunised without the need for prior identification of their
HLA type or the use of HLA-specific CEA epitope(s). Moreover,
RNA can be extracted from very small amounts of tumour tissue
and encodes the individual array of tumour antigens for that
25 tumour. Studies that utilised autologous dendritic cells that
had been pulsed with either CEA peptides or CEA RNA to stimu-
late isolated T cells from carcinoma patients and healthy do-
nors showed that a CEA-specific CTL response could be elicited
in vitro (Alters SE et al. 1997, Adv Exp Med Biol 417, 519-
30 524; Alters SE et al. 1998, J Immunother 21, 17-26; Nair SK et
al. 1999, Int J Cancer 82, 121-124). Another method of gene-
rating immunogenic vaccines is to fuse whole tumour cells di-

rectly to dendritic cells, using an electrofusion technique.
In a pilot study involving patients who had renal cell carci-
noma, the administration of a fusion vaccine composed of
autologous renal cell carcinoma cells fused to allogeneic den-
5 dritic cells produced a significant clinical response in seven
of the 17 treated patients, four of which showed complete re-
sponses (Kugler A et al. 2000, Nat Med 6, 332-336).

Bacterial vaccines: The delivery of DNA that encodes tumour
antigens to APCs can also be accomplished using live attenu-
10 ated bacteria. The advantages of using bacteria as expression
vectors for foreign antigens include improved antigen presen-
tation, because some bacteria are engulfed (taken up) by
phagosomes, resulting in the presentation of inserted antigens
by both MHC class I and class II pathways. Bacteria also pro-
15 vide the requisite transcriptional and translational machinery
for the expression of foreign genes. In bacteria, post-trans-
lational glycosylation of encoded proteins might be proble-
matic. However, as most vaccines aim to elicit a T-cell re-
sponse that is dependent on the MHC class I or class II path-
20 way, the presentation of peptides should not be restricted.
Another advantage of bacterial vectors is that they are sensi-
tive to antibiotics and can be more easily controlled after
administration to patients. Animal studies have shown the
therapeutic effectiveness of using recombinant bacterial vac-
25 cines for the treatment of model tumours; both CD4+- and CD8+-
antigen-specific T-cell responses were generated (Pan ZK et
al. 1995, Nat Med 1, 471-477). Bacteria that are amenable to
the expression of tumour antigens include Bacillus Calmette-
Guerin (BCG), Salmonella typhimurium and Listeria monocyto-
30 genes. Bacterial recombinants that express human tumour anti-
gens have not yet been tested in clinical trials. Although
promising, further research is needed to better characterise

the effects of bacterial vaccines as agents for cancer ther-
apy.

Recombinant viruses: Perhaps the best-studied vaccine develop-
ment method involves the use of recombinant viruses. The most
5 characterised viral system is that of the poxviruses, particu-
larly vaccinia virus. Recombinant vaccinia viruses can accept
a large insert of foreign DNA, replicate accurately, are ea-
sily engineered, allow post-translational modification of for-
eign proteins (e.g. glycosylation), stimulate strong immune
10 responses, and have been extensively used in the human popula-
tion to prevent and eradicate smallpox. The methods for con-
structing recombinant vaccinia viruses have been well de-
scribed, and several different tumour antigens have now been
placed into these viruses, including CEA (Mackett M *et al.*
15 1982, PNAS USA **79**, 7415-7419; Kaufman H *et al.* 1991, Int J
Cancer **48**, 900-907).

In a colon carcinoma model in mice, vaccinia virus expressing
CEA was found to be effective in treating established CEA-ex-
pressing tumours, and was associated with the development of
20 anti-CEA antibody titres and T-cell responses (Kantor J *et al.*
1992, J Natl Cancer Inst **84**, 1084-1091). Interestingly, the
vaccine was most effective in preventing the growth of CEA-
bearing tumours in pre-immunised animals. The same vaccine has
also been tested for safety and immunogenicity in a non-human
25 primate model; toxicity was found to be minimal and the mon-
keys produced CEA-specific T-cell responses after vaccination
(Kantor J. *et al.* 1992, Cancer Res **52**, 6917-6925).

Several clinical trials using recombinant vaccinia vaccine
containing the CEA gene to treat patients who had advanced
30 CEA-expressing tumours have provided evidence that vaccination

was safe even when high titres of virus were given; CEA-spe-
cific T-cell growth and cytotoxicity was also induced.

To circumvent the neutralising antibody responses against the
vaccines that are induced in individuals previously subjected
5 to vaccinia virus vaccination, attention has now focused on
the use of attenuated vaccinia viruses and non-replicating
poxviruses, such as the avipoxviruses. The attenuated vaccinia
strains, such as NYVAC and modified vaccinia virus Ankara
(MVA), contain multiple gene deletions, which prevent the vi-
10 rus from replicating in mammalian cells. Although avipoxvi-
ruses, including fowlpox and canarypox (ALVAC) virus, are
pathogenic in birds, they are also unable to replicate in mam-
malian cells. However, they are able to elicit strong T-cell
immune responses in both rodent models and humans. These T-
15 cell responses have not been accompanied by the induction of
strong neutralising antibodies and have allowed repeated immu-
nisations. An ALVAC virus expressing CEA has shown therapeutic
effectiveness in a CEA tumour model in mice, and has been
tested in human clinical trials (Long L et al. 1999, Curr.
20 Opin. Mol. Ther. 1, 57-63; Marshall JL et al. 1999, J Clin On-
col 17, 332-337).

The safety of viral vaccines and the ability to generate CEA-
specific T-cell responses has led to several novel approaches
for improving the clinical effectiveness of the vaccines. This
25 includes the addition of adjuvants, such as cytokines and co-
stimulatory molecules, to the treatment regimen, and combining
different viruses in a 'prime and boost' strategy.

Attempts to enhance known CEA cancer vaccines: Several ap-
proaches for vaccine design have been presented; however, the
30 results from clinical trials have thus far been disappointing.

One reason might be the use of vaccines in patients who have advanced disease, because they are less likely to elicit a measurable and protective immune response. Although such individuals may be able to respond to common antigens (e.g. influenza or tetanus), their response may be locally immunosuppressed at the tumour site. Thus, patients who have advanced cancers may be less likely to respond to vaccination against a tumour-associated antigen. Several strategies could be employed to improve the ability of CEA vaccines to induce immune response.

Cytokines: IL-2 was the first cytokine to be shown to induce tumour regression in an animal model and it has been tested against a variety of human cancers, and has been shown to have therapeutic potential when administered intravenously as a single agent for metastatic melanoma and renal cell carcinoma. Because vaccines can induce T-cell responses, it seems logical that IL-2 could be used to amplify the initial response, improving the therapeutic effects of cancer vaccines. This has been confirmed experimentally in a mouse model, whereby IL-2 significantly augmented the anti-tumour responses of a vaccinia virus expressing CEA (McLaughlin JP et al. (1996, Cancer Res 56, 2361-2367).

Recombinant viral vaccines that encode both tumour antigen and cytokine genes have been constructed. These have been designed to induce the local release of cytokine at the site of T-cell activation, and should limit the systemic toxicity usually induced by the intravenous administration of high doses of IL-2.

The combination of numerous other cytokines with antigen-specific vaccines has improved the effects of tumour treatment methods. IL-12 is a cytokine that is involved in the stimula-

tion of natural killer cells and the differentiation of naive
T cells. Thus, IL-12 can be considered as an important media-
tor of the effector phase of cellular immunity. Other cyto-
kines that have been evaluated for their ability to augment
5 tumour vaccines include GM-CSF, IFN-γ, tumour necrosis factor α
(TNF-α), interleukin 3 (IL-3), IL-4 and interleukin 10 (IL-
10). GM-CSF has been shown to promote the growth and activa-
tion of dendritic cells, thus improving the antigen presenta-
tion 'arm' of the immune system. Irradiated tumour cells that
10 were transduced ex vivo with the GM-CSF gene have been used as
an autologous cellular vaccine and increased the anti-tumour
T-cell response..

Co-stimulation of tumour-antigen-specific T cells: The activa-
tion of antigen-specific T cells, leading to cytokine produc-
15 tion and proliferation, requires two separate signals. The
first signal is delivered to the T-cell receptor upon recogni-
tion of the peptide-MHC complex. The second signal can be de-
livered by CD28 molecules expressed on T cells after the en-
gagement of the B7 co-stimulatory molecule expressed by acti-
20 vated APCs. The importance of co-stimulation has been demon-
strated by experiments that show that T cells do not respond
when peptide-MHC or TCR recognition takes place in the absence
of co-stimulatory molecules. Other studies have shown that tu-
mour cells can escape detection and subsequent elimination by
25 T cells by the downregulation of co-stimulatory molecules on
the tumour cell surface, or on dendritic cells presenting the
tumour antigens.

The B7 co-stimulatory molecules are homodimeric (*i.e.* express
two identical, intertwined chains of the same protein) members
30 of the immunoglobulin supergene family; they are found on the
surface of cells that are capable of stimulating T-cell acti-

vation and proliferation. B7 molecules can bind to either CD28
or CTLA-4 on the surface of T cells. In the first instance,
the ligation of CD28 (e.g. via B7 molecules or anti-CD28 mono-
clonal antibody) delivers an activating signal to the T cell,
5 which induces the release of cytokines. After activation, T
cells upregulate the expression of CTLA-4 on their cell sur-
face, which also binds B7 molecules but delivers a negative
signal, rendering the T cells less sensitive to further stimu-
lation. The fate of T cells that respond to an antigenic
10 stimulus depends on the balance between the stimulatory and
inhibitory signals delivered to the T cell via these surface
receptors. Likewise, T-cell activation can be enhanced by se-
lectively stimulating CD28 or blocking CTLA-4 activity, and it
can be inhibited by the reverse treatments.

15 Using a mouse model, a mixture of vaccinia viruses expressing
CEA and B7 molecules resulted in enhanced CEA-specific CTL re-
sponses and more-effective anti-tumour activity (Hodge JW *et
al.* 1995, Cancer Res **55**, 3598-3603). This and other findings
support the use of B7 molecules as a vaccine adjuvant, and
20 suggest that this approach will be safe and might be expected
to elicit more-objective clinical responses in larger clinical
trials involving patients whose disease is at an earlier
stage.

Interactions between CD40 and CD40 ligand (also known as CD40L
25 or CD154) represent another co-stimulatory system that has
been widely studied. The CD40 receptor is a 48-kDa protein,
which is found on many cell types, especially APCs, such as B
cells, dendritic cells, macrophages, monocytes, fibroblasts
and endothelial cells. CD40L is a 39-kDa protein that belongs
30 to the TNF family and is predominantly expressed on activated
CD4+ T cells. Interactions between CD40 and CD40L are impor-

21

tant for priming CTLs by CD4+ T cells, and might also help in-
duce humoral immunity. To date, the potential benefits of in-
creasing the expression of CD40L together with that of CEA to
produce a novel tumour vaccine (i.e. vaccinia virus encoding
5   CD40L and CEA) have not been experimentally evaluated.

Prime and boost strategies: The generation of multiple vectors
for vaccination, and the development of neutralising antibo-
dies that prevent repetitive exposure to a single vector, has
led to the use of prime and boost strategies. Such protocols
10 prime the immune response with one vector expressing an anti-
gen, and then boost with a different vector expressing the
same antigen. Heterologous boosting of mice using first vac-
cinia virus and then ALVAC virus expressing CEA improved tu-
mour responses and CTL activity against CEA, compared to those
15 produced by vaccination with either virus alone (Hodge JW *et
al.* 1997, Vaccine **15**, 759-768) and clinical trials are begin-
ning to suggest similar results (Cole DJ *et al.* 1996, Hum Gene
Ther **7**, 1381-1394).

Induction of T-cell help – mechanisms: Presentation of anti-
20 gens has dogmatically been thought of as 2 discrete pathways,
a class II exogenous and a class I endogenous pathway.

Briefly, a foreign protein from outside the cell or from the
cell membrane is taken up by the APC as an endosome that fuses
with an intracellular compartment containing proteolytic en-
25 zymes and MHC class II molecules. Some of the produced pep-
tides bind to class II, which then are translocated to the
cell membrane.

The class I endogenous pathway is characterised by the predo-
minant presentation of cytosolic proteins. This is believed to
30 occur by proteasome-mediated cleavage followed by transporta-

tion of the peptides into the endoplasmic reticulum (ER) via
TAP molecules located in the membrane of the ER. In ER the
peptides bind to class I followed by transportation to the
plasma membrane.

5 However, these 2 pathways are not fully distinct. For example
it is known that dendritic cells and to some extend macro-
phages are capable of endocytosing (pinocytosing) extracellu-
lar proteins and subsequently present them in the context of
MHC class I. It has also previously been demonstrated that u-
10 sing specialised administration routes, e.g. by coupling to
iron oxide beads, exogenous antigens are capable of entering
the Class I pathway. This mechanism seems central, because of
the importance of a concomitant expression of both class I and
class II on the same APC to elicit a three cell type cluster.
15 This three-cell type cluster of interaction has been proposed
by Mitchison (1987) and later by other authors. They showed
the importance of concomitant presentation of class I and
class II epitopes on the same APC. According to the recently
described mechanism for CTL activation (cf. Lanzavecchia,
20 1998, Nature **393**: 413, Matzinger, 1999, Nature Med. **5**: 616,
Ridge *et al.*, 1998, Nature **393**: 474, Bennett *et al.*, 1998, Na-
ture **393**: 478, Schoenberger *et al.*, 1998, Nature **393**: 480,
Ossendrop *et al.*, 1998, J. Exp. Med **187**: 693, and Mackey *et
al.*, 1998, J. Immunol **161**: 2094), professional APCs presenting
25 antigen on MHC class II are recognized by T helper cells. This
results in an activation of the APC (mediated by interaction
by CD40L on the T helper cell and CD40 on the APC). This en-
ables the APC to directly stimulate CTLs that are thereby ac-
tivated. Cf. also Fig. 2 in WO 00/20027.

30 It has previously been demonstrated that insertion of a fo-
reign MHC class II restricted T helper cell epitope into a

self-antigen results in the provision of an antigen capable of inducing strong cross-reactive antibody responses directed against the non-modified self-antigen (cf. WO 95/05849). It was shown that the autoantibody induction is caused by spe-
5 cific T cell help induced by the inserted foreign epitope.

Later, it was concluded that modified self-antigens - with the aid of appropriate adjuvants - ought to be capable of also inducing strong CTL responses against MHC class I restricted self-epitopes and hence the technology described in WO
10 95/05849 can be adapted to also provide vaccination against intracellular and other cell-associated antigens which have epitopes presented in the context of MHC Class I - this concept is the subject matter of WO 00/20027 which is hereby incorporated by reference herein.

15 WO 00/20027 mentions CEA as one putative vaccine target but provides no specific information concerning optimal localisation of foreign T_H epitopes within the CEA amino acid sequence.

As will appear from the above discussion of CEA, this particular polypeptide antigen appears to be a safe target for active
20 immunotherapy. However, there is still a definite need to improve the technology for inducing an immune response against this particular antigen.

OBJECT OF THE INVENTION

It is an object of the present invention to provide improved
25 methods and agents for inducing immune responses in host organisms against cells, especially malignant cells that harbour CEA. It is a further object to provide a method for preparing polypeptide analogues of CEA, analogues that are capable of

inducing an effective immune response against CEA and cells
that harbour CEA.

SUMMARY OF THE INVENTION

The inventors have in part based the present invention on the
5 teachings of WO 00/20027 and WO 95/05849 that teach generally
applicable methods for providing CTL and antibody responses,
respectively, against autologous proteinaceous antigens.

Using the technology disclosed in WO 00/20027, the modified
CEA could be presented by MHC class I as well as by MHC class
10 II molecules on professional antigen presenting cells. Co-
presentation of subdominant self-epitopes on MHC class I and
immunodominant foreign epitopes on MHC class II molecules will
mediate a direct cytokine help from activated MHC class II re-
stricted T-helper cells to MHC class I restricted CTLs (Fig. 2
15 in WO 00/20027). Further, presentation by B-cells of foreign T_H
epitopes present in variants of CEA will result in induction
of production of anti-CEA antibodies, cf. Fig. 1 in WO
00/20027. Hence both strategies as well as their combination
will lead to a specific break of the T cell autotolerance to-
20 wards CEA, thus rendering possible both CTL as well as anti-
body induction that will specifically target CEA.

The present invention is therefore based on a careful study of
the structure of native CEA in order to facilitate the design-
ing of variants of CEA that will prove to be most efficient in
25 breaking tolerance to this antigen. The thus obtained CEA
variants are the *sine qua non* constituents in therapy against
CEA expressing cancers, but of course all technologies dis-
cussed above in the "Background of the Invention" section can
be advantageously combined with the present invention. There-

fore, the technologies discussed in said section are all
incorporated by reference herein.

In conclusion, a vaccine constructed using both of the tech-
nologies outlined above will induce a humeral autoantibody re-
5 sponse with secondary activation of complement and antibody
dependent cellular cytotoxicity (ADCC) activity. Equally
important, it will also induce a cytotoxic T cell response di-
rected against autologous CEA producing cells.

Hence, in the broadest and most general scope, the present in-
10 vention relates to a method for inducing an immune response
against autologous carcinoembryonic antigen (CEA) in an ani-
mal, including a human being, the method comprising effecting
uptake and processing by antigen presenting cells (APCs) in
the animal of at least one modified CEA polypeptide or of a
15 nucleic acid encoding the modified CEA polypeptide or of a
pharmaceutically acceptable microorganism or virus expressing
the modified CEA polypeptide, said at least one modified CEA
polypeptide comprising

- at least about 80 CEA-derived amino acids, either in the
20   form of at least about 80 consecutive CEA-derived amino
         acids or in the form of at least about 80 amino acids
         constituted of uninterrupted CEA-derived CTL epitopes,
         and

- at least one first T helper epitope (T_H epitope) foreign
25   to the animal,

thereby inducing a CTL response and/or an antibody response
that targets the autologous CEA.

Furthermore, the invention relates to certain specific immuno-
genic constructs based on human CEA as well as to compositions
containing these constructs.

Finally, the invention relates to nucleic acid fragments, vec-
5 tors, transformed cells and other tools useful in molecular
biological methods for the production of the analogues of CEA.

LEGENDS TO THE FIGURE

Fig. 1: Overview of the design strategy for the modified CEA
polypeptides of the present invention.
10 The panel to the left shows a model of CEA with domains 1-7
numbered. The N-terminal of the molecule is at the top, the C-
terminus at the bottom. Circles indicate introduction points
for T_H epitopes in the loops of the 7 domains. Arrows indicate
introduction points in the "linkers" between the domains. Tri-
15 angles show the C- and N-terminal introduction points. The
column with heading "struct. design" indicates the optimal in-
troduction regions/points from a strict structural viewpoint,
whereas the column headed "MHC Class I corr." indicates the
chosen introduction regions/points after an analysis of possi-
20 ble interference with CTL epitopes of CEA. Asterisks indicate
that the introduction region includes a glycosylation point.

Fig. 2: Schematic overview of 4 preferred CEA variants.
The panel to the left shows a schematic view of the CEA do-
mains and the 4 models schematically show the variants having
25 the amino acid sequences set forth in SEQ ID NOs: 6, 8, 10,
and 12, respectively.

DETAILED DISCLOSURE OF THE INVENTION

Definitions

In the following a number of terms used in the present specification and claims will be defined and explained in de-
5   tail in order to clarify the metes and bounds of the invention.

An "autologous CEA" is in the present specification and claims intended to denote a CEA polypeptide of an animal that is going to be vaccinated against its own CEA. In other words, the
10 term is only relevant when the relation to the animal that it going to be vaccinated is considered.

The terms "T-lymphocyte" and "T-cell" will be used interchangeably for lymphocytes of thymic origin which are responsible for various cell mediated immune responses as well as
15 for effector functions such as helper activity in the humeral immune response. Likewise, the terms "B-lymphocyte" and "B-cell" will be used interchangeably for antibody-producing lymphocytes.

An "antigen presenting cell" (APC) is a cell which presents
20 epitopes to T-cells. Typical antigen-presenting cells are macrophages, dendritic cells and other phagocytizing and pinocytizing cells. It should be noted that B-cells also functions as APCs by presenting T_H epitopes bound to MCH class II molecules to T_H cells but when generally using the term APC in the
25 present specification and claims it is intended to refer to the above-mentioned phagocytizing and pinocytizing cells.

"Helper T-lymphocytes" or "T_H cells" denotes CD4 positive T-cells which provide help to B-cells and cytotoxic T-cells via

the recognition of T_H epitopes bound to MHC Class II molecules on antigen presenting cells.

The term "cytotoxic T-lymphocyte" (CTL) will be used for CD8 positive T-cells which require the assistance of T_H cells in
5 order to become activated.

A "specific" immune response is in the present context intended to denote a polyclonal immune response directed predominantly against a molecule or a group of quasi-identical molecules or, alternatively, against cells which present CTL epi-
10 topes of the molecule or the group of quasi-identical molecules.

The term "polypeptide" is in the present context intended to mean both short peptides of from 2 to 10 amino acid residues, oligopeptides of from 11 to 100 amino acid residues, and poly-
15 peptides of more than 100 amino acid residues. Furthermore, the term is also intended to include proteins, i.e. functional biomolecules comprising at least one polypeptide; when comprising at least two polypeptides, these may form complexes, be covalently linked, or may be non-covalently linked. The poly-
20 peptide(s) in a protein can be glycosylated and/or lipidated and/or comprise prosthetic groups.

The term "subsequence" means any consecutive stretch of at least 3 amino acids or, when relevant, of at least 3 nucleo-tides, derived directly from a naturally occurring amino acid
25 sequence or nucleic acid sequence, respectively.

The term "animal" is in the present context in general intended to denote an animal species (preferably mammalian), such as Homo sapiens, Canis domesticus, etc. and not just one single animal. However, the term also denotes a population of

such an animal species, since it is important that the indi-
viduals immunized according to the method of the invention all
harbour substantially the same CEA allowing for immunization
of the animals with the same immunogen(s). If, for instance,
5 genetic variants of CEA exist in different human populations
it may be necessary to use different immunogens in these dif-
ferent populations in order to be able to break the autotole-
rance towards the CEA in each population.

By the term "down-regulation a autologous CEA" is herein meant
10 reduction in the living organism of the amount and/or activity
of CEA. The down-regulation can be obtained by means of seve-
ral mechanisms including removal of the CEA by scavenger cells
(such as macrophages and other phagocytizing cells), and even
more important, that cells carrying or harbouring the antigen
15 are killed by CTLs in the animal.

The expression "...consecutive CEA-derived amino acids..." is in-
tended to denote amino acids that can be found in the same se-
quential order in the primary structure of a naturally occur-
ring CEA, nevertheless allowing for conservative substitutions
20 that do not change the immunologic properties of such a CEA
sequence.

The expression "...amino acids constituted of uninterrupted CEA-
derived CTL epitopes..." is meant a stretch of amino acids that
can be subdivided into shorter consecutive stretches of CEA
25 that each constitute a CTL epitope found in naturally occur-
ring CEA. Again, the language allows for minor, insignificant
changes in the amino acid sequences of these CTL epitopes, as
long as the CTL epitopes are not rendered less immunoreactive
than their natural form.

The expression "effecting simultaneous presentation by a suit-
able APC" is intended to denote that the animal's immune sys-
tem is subjected to an immunogenic challenge in a controlled
manner which results in the simultaneous presentation by APCs
5 of the CEA epitopes and foreign epitopes in question. As will
appear from the disclosure below, such challenge of the immune
system can be effected in a number of ways of which the most
important are vaccination with polypeptide containing "phar-
maccines" (i.e. a vaccine which is administered to treat or
10 ameliorate ongoing disease) or nucleic acid "pharmaccine" vac-
cination. The important result to achieve is that immune com-
petent cells in the animal are confronted with APCs displaying
the relevant epitopes in an immunologically effective manner.

The term "immunogen" is intended to denote a substance which
15 is capable of inducing an immune response in a certain animal.
It will therefore be understood that autologous CEA is not an
immunogen in the autologous host – it is necessary to use ei-
ther a strong adjuvant and/or to co-present T helper epitopes
with the autologous CEA in order to mount an immune response
20 against autologous CEA and in such a case the "immunogen" is
the composition of matter which is capable of breaking
autotolerance.

The term "immunogenically effective amount" has its usual
meaning in the art, i.e. an amount of an immunogen which is
25 capable of inducing an immune response which significantly en-
gages pathogenic agents which share immunological features
with the immunogen.

The term "pharmaceutically acceptable" has its usual meaning
in the art, i.e. it is used for a substance that can be ac-
30 cepted as part of a medicament for human use when treating the

disease in question and thus the term effectively excludes the use of highly toxic substances that would worsen rather than improve the treated subject's condition.

When using the expression that the autologous CEA has been
5 subjected to a "modification" is herein meant a chemical modification of the polypeptide which constitutes at least part of one of the 7 domains of autologous CEA. Such a modification can e.g. be derivatization (e.g. alkylation) of certain amino acid residues in the amino acid sequence, but as will be ap-
10 preciated from the disclosure below, the preferred modifications comprise changes of the primary structure of the amino acid sequence.

When discussing "tolerance" and "autotolerance" is understood that since CEA molecules which are the targets of the present
15 inventive method are self-proteins in the population to be vaccinated, normal individuals in the population do not mount an immune response against CEA. It cannot be excluded, though, that occasional individuals in an animal population might be able to produce antibodies against the autologous CEA, e.g. as
20 part of a autoimmune disorder. At any rate, an animal will normally only be autotolerant towards its own CEA, but it cannot be excluded that analogues derived from other animal species or from a population having a different phenotype would also be tolerated by said animal.

25 A "foreign T-cell epitope" is a peptide which is able to bind to an MHC molecule and which stimulates T-cells in an animal species. Preferred foreign epitopes are "promiscuous" epitopes, i.e. epitopes which binds to a substantial fraction of MHC class II molecules in an animal species or population. A
30 term which is often used interchangeably in the art is the

term "universal T-cell epitopes" for this kind of epitopes.
Only a very limited number of such promiscuous T-cell epitopes
are known, and they will be discussed in detail below. It
should be noted that in order for the immunogens which are
5   used according to the present invention to be effective in as
large a fraction of an animal population as possible, it may
be necessary to 1) insert several foreign T-cell epitopes in
the same analogue or 2) prepare several analogues wherein each
analogue has a different promiscuous epitope inserted. It
10 should be noted that the concept of foreign T-cell epitopes
also encompasses use of cryptic T-cell epitopes, *i.e.* epitopes
which are derived from a self-protein and which only exerts
immunogenic behaviour when existing in isolated form without
being part of the self-protein in question.

15 A "foreign T helper lymphocyte epitope" (a foreign T_H epitope)
is a foreign T cell epitope which binds an MHC Class II mole-
cule and can be presented on the surface of an antigen pre-
senting cell (APC) bound to the MHC Class II molecule. It is
also important to add that the "foreignness" feature therefore
20 has two aspects: A foreign T_H epitope is 1) presented in the
MHC Class II context by the animal in question and 2) the for-
eign epitope is not derived from the same polypeptide as the
target antigen for the immunization – the epitope is thus also
foreign to the target antigen.

25 A "CTL epitope" is a peptide which is able to bind to an MHC
class I molecule.

A "functional part" of a (bio)molecule is in the present con-
text intended to mean the part of the molecule which is re-
sponsible for at least one of the biochemical or physiological
30 effects exerted by the molecule. It is well-known in the art

that many enzymes and other effector molecules have an active site which is responsible for the effects exerted by the molecule in question. Other parts of the molecule may serve a stabilizing or solubility enhancing purpose and can therefore be

5 left out if these purposes are not of relevance in the context of a certain embodiment of the present invention. For instance it is possible to use certain cytokines as a modifying moiety in the modified CEA (cf. the detailed discussion below), and in such a case, the issue of stability may be irrelevant since

10 the coupling to the modified CEA provides the stability necessary.

The term "adjuvant" has its usual meaning in the art of vaccine technology, i.e. a substance or a composition of matter which is 1) not in itself capable of mounting a specific im-

15 mune response against the immunogen of the vaccine, but which is 2) nevertheless capable of enhancing the immune response against the immunogen. Or, in other words, vaccination with the adjuvant alone does not provide an immune response against the immunogen, vaccination with the immunogen may or may not

20 give rise to an immune response against the immunogen, but the combined vaccination with immunogen and adjuvant induces an immune response against the immunogen which is stronger than that induced by the immunogen alone.

"Targeting" of a molecule is in the present context intended

25 to denote the situation where a molecule upon introduction in the animal will appear preferentially in certain tissue(s) or will be preferentially associated with certain cells or cell types. The effect can be accomplished in a number of ways including formulation of the molecule in composition facilita-

30 ting targeting or by introduction in the molecule of groups

which facilitates targeting. These issues will be discussed in detail below.

"Stimulation of the immune system" means that a substance or composition of matter exhibits a general, non-specific immu-
5 nostimulatory effect. A number of adjuvants and putative adju-vants (such as certain cytokines) share the ability to stimu-late the immune system. The result of using an immunostimula-ting agent is an increased "alertness" of the immune system meaning that simultaneous or subsequent immunization with an
10 immunogen induces a significantly more effective immune re-sponse compared to isolated use of the immunogen

Preferred embodiments

The present invention targets CEA via Active Specific Immuno-therapy – in essence this can be achieved by stimulating ei-
15 ther or both of the two arms of the immune system. Since CEA is a membrane bound protein that is exposed mostly to the ex-tracellular phase and thereby open for antibody interaction, it is expedient to raise an antibody response against CEA, *i.e.* a humoral response. On the other hand, as discussed
20 above, cell-mediated immunity (e.g. a CTL response) against CEA-bearing cells should also be a feasible means of attacking this particular antigen and diseases related thereto.

According to the invention, it is therefore possible to 1) use an immunogen that induces CTLs reactive with CEA as well as
25 antibodies reactive with CEA, 2) use an immunogen that only induces CTLs reactive with CEA, 3) use an immunogen that only induces antibodies reactive with CEA, or use a combination of 2 and 3 (which both can be combined with 1).

From a practical viewpoint, it is interesting to include a
large fraction of CEA epitopes. So, even though it is believed
to be sufficient to include down to about 80 CEA-derived amino
acids, longer parts of CEA are preferred: at least about 100,
5 120, 140, 160, 180, 200, 220, 250, 300, 350, 400, 450, 500,
550, 600, 650, 700, thus even up to about the full sequence of
CEA. However, since the molecule consists of domains (each
having a length of about 100 amino acids) it is especially
preferred to substantially include the amino acid sequence of
10 at least one domain, such as at least 2, 3, 4, 5, 6 or even
all 7 domains of CEA (still allowing for the minor variations
discussed above). The domains of CEA are consecutively num-
bered from the N-terminus of the molecule. To "substantially
include" means in this context that the amino acid sequence of
15 such a domain may be subjected to minor variations in the form
of conservative substitutions that will not significantly al-
ter the immunologic profile of such a domain. The term also
means, that in the event a foreign T_H epitope is introduced ac-
cording to the invention in a domain region, this is done in a
20 manner that will not significantly interfer with the 3-dimen-
sional structure of the domain region (this can e.g. be
achieved by introducing the epitope in the loop in one or more
of the domains, cf. below. It is important to note that if it
is desired to merely induce CTL responses, the requirement of
25 preservation of 3-dimensional structure of one or more domains
is irrelevant.

In order to induce a CTL response against a cell which pre-
sents epitopes derived from the autologous CEA on its surface,
it is normally necessary that at least one CTL epitope, when
30 presented, is associated with an MHC Class I molecule on the
surface of the APC. Furthermore it is preferred that the at

least one first foreign T_H epitope, when presented, is associated with an MHC Class II molecule on the surface of the APC.

Preferred APCs presenting the CTL epitopes are dendritic cells and macrophages, but any pino- or phagocytizing APC which is

5   capable of simultaneously presenting 1) CTL epitopes bound to MHC class I molecules and 2) T_H epitopes bound to MHC class II molecules, is a preferred APC according to the invention.

Normally, it will be advantageous to confront the immune system with a large fraction of the amino acid sequence of the

10 autologous CEA – this will ensure that a large number of CTL epitopes and/or B-cell epitopes will be present in the agent that is taken up by the APC. Hence, in a preferred embodiment, the modified CEA polypeptide is in the form of at least one first analogue of the autologous CEA, said first analogue con-

15 taining autologous CEA-derived CTL epitope(s), and the at least first foreign T_H epitope.

In order to maximize the chances of mounting an effective immune response, it is preferred that the above-mentioned first analogue contains a substantial fraction of known and pre-

20 dicted CTL epitopes of autologous CEA, i.e. a fraction of the known and predicted CTL epitopes which binds a sufficient fraction of MHC Class I molecules in a population. For instance, it is preferred that the substantial fraction of known and predicted CTL epitopes in the amino acid sequence of the

25 analogue are recognized by at least 50% of the MHC-I haplotypes recognizing all known and predicted CTL epitopes in the autologous CEA, but higher percentages are preferred, such as at least 60, at least 70, at least 80, and at least 90%. Especially preferred is the use of analogues, which preserve sub-

30 stantially all known CTL epitopes of the autologous CEA are

present in the analogue, *i.e.* close to 100% of the known CTL
epitopes. Accordingly, it is also especially preferred that
substantially all predicted CTL epitopes of the autologous CEA
are present in the at least first analogue.

5 The above-indicated approach renders possible the mounting of
a CTL response against all parts of cell-associated CEA, in-
cluding the membrane-anchoring region and also regions of CEA
that are in close proximity to the cell membrane and therefore
may be shielded by other cellular molecules, thereby making
10 these regions less effective as targets for humoral immune re-
sponses.

Methods for predicting the presence of CTL epitopes are well-
known in the art, cf. e.g. Rothbard *et al.* EMBO J. 7:93-100
(1988) and Rammensee HG *et al.* 1995, Immunogenetics **41**, 178-
15 228. Furthermore, a number of CTL epitopes have already been
identified in CEA.

As will be apparent from the present specification and claims
it is expected that the inventive method described herein will
render possible the effective induction of CTL responses
20 against autologous CEA.

Since CEA is a membrane-associated antigen, it is according to
the present invention also advantageous to induce an antibody
response while at the same time inducing CTL mediated immu-
nity, cf above. However, when raising a humeral immune re-
25 sponse against autologous CEA it is preferred to substantially
restrict the antibody response to interaction with the parts
of the antigen that are normally exposed to possible interac-
tion with antibodies (*i.e.* those regions being relatively re-
mote from the cell membrane). Otherwise the result could pos-
30 sibly be the induction of an antibody response against parts

of the antigen which is not normally engaging the humeral im-
mune system, and this will in turn increase the risk of indu-
cing cross-reactivity with antigens not related to any patho-
logy - even though this is not regarded a serious risk, the
5 size of CEA renders truncated forms of the molecule likely
candidates for a vaccine. One elegant way of obtaining this
restriction is to perform nucleic acid vaccination with an
analogue of autologous CEA, where the extracellular part
thereof is either unaltered or includes a T_H epitope which does
10 not substantially alter the 3D structure of the relevant ex-
tracellular part of the antigen. As one possible alternative,
immunization can be performed with both a CTL directed immuno-
gen and a B-cell directed immunogen where the B-cell directed
immunogen is substantially incapable of effecting immunization
15 against the cell-proximal part part of the target antigen (the
B-cell directed immunogen could e.g. include only the first 3
domains of CEA - domains 2, 4 and 6 share a very high homology
and the same is true fo for domain 3, 5 and 7 and the inclu-
sion of the first 3 domains therefore ought to provide the de-
20 sired variability with respect to B-cell epitopes in the immu-
nogen).

Induction of antibody responses can be achieved in a number of
ways known to the person skilled in the art. For instance, the
at least one first analogue may comprise at least one CEA B-
25 cell epitope, so that immunization of the animal with the
first analogue also induces production of antibodies in the
animal against the autologous CEA - this type of analogue is
as mentioned above very well suited for nucleic acid vaccina-
tion. Alternatively, the method of the invention can involve
30 effecting presentation to the animal's immune system of an im-
munogenically effective amount of at least one *second* analogue
(which shares the generic definition of a "modified CEA poly-

peptide" used herein). A convenient way to achieve that the
second analogue has the desired antibody-inducing effect is to
include at least one second foreign T_H epitope in the second
analogue, i.e. a strategy like the one used for the first ana-
5 logue. This at least one second T_H epitope may be the same or
different from the at least one first T_H epitope.

In the cases where it is desired to also mount an effective
humoral immune response, it is advantageous that the first
and/or second analogue(s) comprise(s) a substantial fraction
10 of the B-cell epitopes of autologous CEA, especially a sub-
stantial fraction of such B-cell epitopes which are exposed to
antibody interaction in the naturally occurring form of
autologous, membrane bound CEA, cf. the above discussion of
the region including domains 1-3.

15 The above-discussed variations and modifications of the
autologous CEA can take different forms. It is preferred that
the variation and/or modification involves amino acid substi-
tution and/or deletion and/or insertion and/or addition. These
fundamental operations relating to the manipulation of an
20 amino acid sequence are intended to cover both single-amino
acid changes as well as operations involving stretches of
amino acids (i.a. shuffling of amino acid stretches within the
polypeptide antigen; this is especially interesting when only
aiming at inducing CTLs, since only considerations concerning
25 preservation of CTL epitopes are relevant). It will be under-
stood, that the introduction of even as little as one single
amino acid insertion or deletion may give rise to the emer-
gence of a foreign T_H epitope in the sequence of the analogue,
i.e. the emergence of an MHC Class II molecule binding se-
30 quence. However, in most situations it is preferable (and even
necessary) to introduce a known foreign T_H epitope, and such an

operation will require amino acid substitution and/or inser-
tion (or sometimes addition in the form of either conjugation
to a carrier protein or provision of a fusion polypeptide by
means of molecular biology methods). It is preferred that the
5   number of amino acid insertions, deletions, substitutions or
additions is at least 2, such as 3, 4, 5, 6, 7, 8, 9, 10, 11,
12, 13, 14, 15, 16, 17, 18, 19, 20, and 25 insertions, substi-
tutions, additions or deletions. It is furthermore preferred
that the number of amino acid substitutions is not in excess
10 of 150, such as at most 100, at most 90, at most 80, and at
most 70. It is especially preferred that the number of substi-
tutions, insertions, deletions, or additions does not exceed
60, and in particular the number should not exceed 50 or even
40. Most preferred is a number of not more than 36 (correspon-
15 ding to the number of the total number of amino acids in the
P2+P30 epitopes).

The invention requires modification of CEA by introducing at
least one foreign immunodominant T_H epitope. It will be under-
stood that the question of immune dominance of a T-cell epi-
20 tope depends on the animal species in question. As used
herein, the term "immunodominance" simply refers to epitopes
which in the vaccinated individual/population gives rise to a
significant immune response, but it is a well-known fact that
a T-cell epitope which is immunodominant in one individual is
25 not necessarily immunodominant in another individual of the
same species, even though it may be capable of binding MHC-II
molecules in the latter individual. True immune dominant T_H
epitopes are those which, independent of the polypeptide
wherein they form a subsequence, give rise to activation of T_H
30 cells - in other words, some T_H epitopes have, as an intrinsic
feature, the characteristic of substantially never being cryp-
tic since they are substantially always processed by APCs and

presented in the context of an MHC II molecule on the surface
of the APC.

Another important point is the issue of MHC restriction of T-
cell epitopes. In general, naturally occurring T-cell epitopes
5 are MHC restricted, *i.e.* a certain peptides constituting a T-
cell epitope will only bind effectively to a subset of MHC
Class II molecules. This in turn has the effect that in most
cases the use of one specific T-cell epitope will result in a
vaccine component which is only effective in a fraction of the
10 population, and depending on the size of that fraction, it can
be necessary to include more T_H epitopes in the same molecule,
or alternatively prepare a multi-component vaccine wherein the
components are variants of the antigen, which are distin-
guished from each other by the nature of the T-cell epitope
15 introduced.

If the MHC restriction of the T-cells used is completely un-
known (for instance in a situation where the vaccinated animal
has a poorly defined MHC composition), the fraction of the
animal population covered by a specific vaccine composition
20 can be determined by means of the following formula:

$$f_{population} = 1 - \prod_{i=1}^{n}(1 - p_i) \qquad (II)$$

-where p_i is the frequency in the population of responders to
the ith foreign T-cell epitope present in the vaccine composi-
tion, and n is the total number of foreign T-cell epitopes in
25 the vaccine composition. Thus, a vaccine composition contain-
ing 3 foreign T-cell epitopes having response frequencies in
the population of 0.8, 0.7, and 0.6, respectively, would give

$$1 - 0.2 \times 0.3 \times 0.4 = 0.976$$

−*i.e.* 97.6 percent of the population will statistically mount an MHC-II mediated response to the vaccine.

The above formula does not apply in situations where a more or less precise MHC restriction pattern of the peptides used is
5   known. If, for instance a certain peptide only binds the human MHC-II molecules encoded by HLA-DR alleles DR1, DR3, DR5, and DR7, then the use of this peptide together with another peptide which binds the remaining MHC-II molecules encoded by HLA-DR alleles will accomplish 100% coverage in the population
10 in question. Likewise, if the second peptide only binds DR3 and DR5, the addition of this peptide will not increase the coverage at all. If one bases the calculation of population response purely on MHC restriction of T-cell epitopes in the vaccine, the fraction of the population covered by a specific
15 vaccine composition can be determined by means of the following formula:

$$f_{population} = 1 - \prod_{j=1}^{3} (1 - \varphi_j)^2 \qquad (III)$$

−wherein ϕ_j is the sum of frequencies in the population of allelic haplotypes encoding MHC molecules which bind any one of
20 the T-cell epitopes in the vaccine and which belong to the jth of the 3 known HLA loci (DP, DR and DQ); in practice, it is first determined which MHC molecules will recognize each T-cell epitope in the vaccine and thereafter these MHC molecules are listed by type (DP, DR and DQ) − then, the individual fre-
25 quencies of the different listed allelic haplotypes are summed for each type, thereby yielding ϕ_1, ϕ_2, and ϕ_3.

It may occur that the value p_i in formula II exceeds the corresponding theoretical value π_i:

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$$\pi_i = 1 - \prod_{j=1}^{3}(1 - v_j)^2 \qquad\qquad (IV)$$

-wherein v_j is the sum of frequencies in the population of al-
lelic haplotypes encoding MHC molecules which bind the ith T-
cell epitope in the vaccine and which belong to the jth of the

5   3 known HLA loci (DP, DR and DQ). This means that in $1-\pi_i$ of
the population there is a frequency of responders of
$f_{residual\_i} = (p_i-\pi_i)/(1-\pi_i)$. Therefore, formula III can be ad-
justed so as to yield formula V:

$$f_{population} = 1 - \prod_{j=1}^{3}(1 - \varphi_j)^2 + \left(1 - \prod_{i=1}^{n}(1 - f_{residual\_i})\right) \qquad (V)$$

10   -where the term $1-f_{residual\_i}$ is set to zero if negative. It
should be noted that formula V requires that all epitopes have
been haplotype mapped against identical sets of haplotypes.

Therefore, when selecting T-cell epitopes to be introduced in
the modified CEA polypeptide, it is important to include all

15   knowledge of the epitopes which is available: 1) The frequency
of responders in the population to each epitope, 2) MHC re-
striction data, and 3) frequency in the population of the
relevant haplotypes.

There exist a number of naturally occurring "promiscuous" T-

20   cell epitopes which are active in a large proportion of indi-
viduals of an animal species or an animal population and these
are preferably introduced in the vaccine thereby reducing the
need for a very large number of different modified CEAs in the
same vaccine.

25   The promiscuous epitope can according to the invention be a
naturally occurring human T-cell epitope such as epitopes from
tetanus toxoid (e.g. the P2 and P30 epitopes, cf. SEQ ID NOs:

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13 and 14, respectively), diphtheria toxoid, Influenza virus
hemagluttinin (HA), and P. falciparum CS antigen.

Over the years a number of other promiscuous T-cell epitopes
have been identified. Especially peptides capable of binding a

5 large proportion of HLA-DR molecules encoded by the different
HLA-DR alleles have been identified and these are all possible
T-cell epitopes to be introduced in modified CEA used accor-
ding to the present invention. Cf. also the epitopes discussed
in the following references which are hereby all incorporated

10 by reference herein: WO 98/23635 (Frazer IH et al., assigned
to The University of Queensland); Southwood S et. al, 1998, J.
Immunol. 160: 3363-3373; Sinigaglia F et al., 1988, Nature
336: 778-780; Rammensee HG et al., 1995, Immunogenetics 41: 4
178-228; Chicz RM et al., 1993, J. Exp. Med 178: 27-47; Hammer

15 J et al., 1993, Cell 74: 197-203; and Falk K et al., 1994, Im-
munogenetics 39: 230-242. The latter reference also deals with
HLA-DQ and -DP ligands. All epitopes listed in these 5 refe-
rences are relevant as candidate natural epitopes to be used
in the present invention, as are epitopes which share common

20 motifs with these.

Alternatively, the epitope can be any artificial T-cell epi-
tope which is capable of binding a large proportion of haplo-
types. In this context the pan DR epitope peptides ("PADRE")
described in WO 95/07707 and in the corresponding paper Alex-

25 ander J et al., 1994, Immunity 1: 751-761 (both disclosures
are incorporated by reference herein) are interesting candi-
dates for epitopes to be used according to the present inven-
tion. It should be noted that the most effective PADRE pep-
tides disclosed in these papers carry D-amino acids in the C-

30 and N-termini in order to improve stability when administered.
However, the present invention primarily aims at incorporating

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the relevant epitopes as part of the modified CEA which should
then subsequently be broken down enzymatically inside the ly-
sosomal compartment of APCs to allow subsequent presentation
in the context of an MHC-II molecule and therefore it is not
5 expedient to incorporate D-amino acids in the epitopes used in
the present invention.

One especially preferred PADRE peptide is the one having the
amino acid sequence AKFVAAWTLKAAA (SEQ ID NO: 15) or an immu-
nologically effective subsequence thereof. This, and other
10 epitopes having the same lack of MHC restriction are preferred
T-cell epitopes which should be present in the modified CEA
used in the inventive method. Such super-promiscuous epitopes
will allow for the most simple embodiments of the invention
wherein only one single modified CEA is presented to the vac-
15 cinated animal's immune system.

The nature of the above-discussed variation/modification pre-
ferably also comprises that

- at least one first moiety is included in the modified
  CEA, said first moiety effecting targeting of the modi-
20 fied CEA to an antigen presenting cell (APC), and/or

- at least one second moiety is included in the modified
  CEA, said second moiety stimulating the immune system,
  and/or

- at least one third moiety is included in the modified
25 CEA, said third moiety optimising presentation thereof to
  the immune system.

The functional and structural features relating these first,
second and third moieties will be discussed in the following,

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but also the general description of such moieties given in the
"Background of the Invention" section above applies here:

They can be present in the form of side groups attached cova-
lently or non-covalently to suitable chemical groups in the
5 amino acid sequence of the autologous CEA or a subsequence
thereof. This is to mean that stretches of amino acid residues
derived from the autologous CEA are derivatized without alter-
ing the primary amino acid sequence, or at least without in-
troducing changes in the peptide bonds between the individual
10 amino acids in the chain.

The moieties can also be in the form of fusion partners to the
amino acid sequence derived from the autologous CEA. In this
connection it should be mentioned that both possibilities in-
clude the option of conjugating the amino acid sequence to a
15 carrier, cf. the discussion of these below. In other words, in
the present context the term "fusion protein is not merely re-
stricted to a fusion construct prepared by means of expression
of a DNA fragment encoding the construct but also to a conju-
gate between two proteins which are joined by means of a pep-
20 tide bond in a subsequent chemical reaction.

As mentioned above, the modified CEA can also include the in-
troduction of a first moiety which targets the modified CEA to
an APC or a B-lymphocyte. For instance, the first moiety can
be a specific binding partner for a B-lymphocyte specific sur-
25 face antigen or for an APC specific surface antigen. Many such
specific surface antigens are known in the art. For instance,
the moiety can be a carbohydrate for which there is a receptor
on the B-lymphocyte or the APC (e.g. mannan or mannose). Al-
ternatively, the second moiety can be a hapten. Also an anti-
30 body fragment which specifically recognizes a surface molecule

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on APCs or lymphocytes can be used as a first moiety (the sur-
face molecule can e.g. be an FCγ receptor of macrophages and
monocytes, such as FCγRI or, alternatively any other specific
surface marker such as CD40 or CTLA-4). It should be noted
5 that all these exemplary targeting molecules can be used as
part of an adjuvant, cf. below. CD40 ligand, antibodies
against CD40, or variants thereof which bind CD40 will target
the modified CEA to dendritic cells. At the same time, recent
results have shown that the interaction with the CD40 molecule
10 renders the T_H cells unessential for obtaining a CTL response.
Hence, it is contemplated that the general use of CD40 binding
molecules as the first moiety (or as adjuvants, cf. below)
will enhance the CTL response considerably; in fact, the use
of such CD40 binding molecules as adjuvants and "first moie-
15 ties" in the meaning of the present invention is believed to
be inventive in its own right.

As an alternative or supplement to targeting the modified CEA
to a certain cell type in order to achieve an enhanced immune
response, it is possible to increase the level of responsive-
20 ness of the immune system by including the above-mentioned
second moiety, which stimulates the immune system. Typical ex-
amples of such second moieties are cytokines, heat-shock pro-
teins, and hormones, as well as effective parts thereof.

Suitable cytokines to be used according to the invention are
25 those which will normally also function as adjuvants in a vac-
cine composition, e.g. interferon γ (IFN-γ), Flt3 ligand
(Flt3L), interleukin 1 (IL-1), interleukin 2 (IL-2), interleu-
kin 4 (IL-4), interleukin 6 (IL-6), interleukin 12 (IL-12),
interleukin 13 (IL-13), interleukin 15 (IL-15), and granulo-
30 cyte-macrophage colony stimulating factor (GM-CSF); alterna-
tively, the functional part of the cytokine molecule may suf-

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fice as the second moiety. With respect to the use of such cy-
tokines as adjuvant substances, cf. the discussion below.

Alternatively, the second moiety can be a toxin, such as lis-
teriolycin (LLO), lipid A and heat-labile enterotoxin. Also, a
5   number of mycobacterial derivatives such as MDP (muramyl
dipeptide), CFA (complete Freund's adjuvant) and the trehalose
diesters TDM and TDE are interesting possibilities.

According to the invention, suitable heat shock proteins used
as the second moiety can be HSP70, HSP90, HSC70 (a heat shock
10   cognate), GRP94, and calreticulin (CRT).

Also the possibility of introducing a third moiety that en-
hances the presentation of the modified CEA to the immune sys-
tem is an important embodiment of the invention. The art has
shown several examples of this principle. For instance, it is
15   known that the palmitoyl lipidation anchor in the *Borrelia*
burgdorferi protein OspA can be utilised so as to provide
self-adjuvating polypeptides (cf. e.g. WO 96/40718). It seems
that the lipidated proteins form up micelle-like structures
with a core consisting of the lipidation anchor parts of the
20   polypeptides and the remaining parts of the molecule protru-
ding therefrom, resulting in multiple presentations of the an-
tigenic determinants. Hence, the use of this and related ap-
proaches using different lipidation anchors (e.g. a myristyl
group, a farnesyl group, a geranyl-geranyl group, a GPI-an-
25   chor, and an N-acyl diglyceride group) are preferred embodi-
ments of the invention, especially since the provision of such
a lipidation anchor in a recombinantly produced protein is
fairly straightforward and merely requires use of e.g. a natu-
rally occurring signal sequence as a fusion partner for the
30   modified CEA, cf. below. Another possibility is use of the C3d

fragment of complement factor C3 or C3 itself (cf. Dempsey et
al., 1996, Science 271, 348-350 and Lou & Kohler, 1998, Nature
Biotechnology 16, 458-462).

In the present context it is of high importance to note that
5 CEA naturally has a GPI anchor, meaning that by preserving
this in the modified molecule, the self-adjuvating effect
would be a possibility. The preservation can e.g. be obtained
by preserving the natural C-terminal signal sequence from the
native CEA encoding sequence (the C-terminal signal sequence
10 spans amino acids 648 through 668 in SEQ ID NO: 2, meaning
that the mature CEA spans amino acids 1-647 in SEQ ID NOs: 2
and 4). By including this known signal sequence also in con-
structs that do not include the C-terminus of CEA, it will be
achieved that the resulting expression product is anchored to
15 the membrane.

However, it is known that expression of membrane bound pro-
teins may be at a lower level than that of a secreted protein,
so also modified versions of CEA that lack the GPI anchor are
embraced by the present invention.

20 It is important to note that when attempting to use the method
of the invention against epitopes of the extracellularly ex-
posed parts of CEA, it is most preferred that the modified CEA
substantially preserves the 3-dimensional structure of one or
more domains of CEA. Thus, in the present specification and
25 claims this is intended to mean that the 3-dimensional struc-
ture of the part of CEA which is extracellularly exposed is
preserved, since, as mentioned above, part of CEA are not ex-
pected to effectively engage the humeral immune system. It is
in this context preferred that the 3D structures of at least 4
30 domains are substantially preserved, especially domains 1-4.

In a particularly preferred embodiment, the 3D structures of
all 7 domains are substantially preserved.

For the purposes of the present invention, it is however suf-
ficient if the variation/modification (be it an insertion, ad-
5   dition, deletion or substitution) gives rise to a foreign T-
cell epitope and at the same time preserves a substantial num-
ber of the CTL epitopes in CEA (and sometimes also a substan-
tial number of B-cell epitopes).

The following formula describes the constructs generally co-
10 vered by the invention:

$$(MOD_1)_{s1}(CEA_{e1})_{n1}(MOD_2)_{s2}(CEA_{e2})_{n2}\ldots(MOD_x)_{sx}(CEA_{ex})_{nx} \qquad (I)$$

-where CEA_{e1}-CEA_{ex} are x CTL and/or B-Cell epitope containing
subsequences of the autologous CEA which independently are
identical or non-identical and which may contain or not con-
15 tain foreign side groups, x is an integer $\geq$ 3, n1-nx are x in-
tegers $\geq$ 0 (at least one is $\geq$ 1), MOD_1-MOD_x are x modifications
introduced between the preserved epitopes, and s1-sx are x in-
tegers $\geq$ 0 (at least one is $\geq$ 1 if no side groups are intro-
duced in the sequences). Thus, given the general functional
20 restraints on the immunogenicity of the constructs as well as
the requirements set forth above, the invention allows for all
kinds of permutations of the original constant CEA sequence,
and all kinds of modifications therein. Thus, included in the
invention are modified CEA obtained by omission of parts of
25 the autologous CEA sequence.

It is furthermore preferred that the variation and/or modifi-
cation includes duplication, when applicable, of the at least
one B-cell epitope, or of at least one CTL epitope of the

autologous CEA. This strategy will give the result that multi-
ple copies of preferred epitopic regions are presented to the
immune system and thus maximizing the probability of an effec-
tive immune response. Hence, this embodiment of the invention
5 utilises multiple presentations of epitopes derived from the
autologous CEA (*i.e.* formula I wherein at least one B-cell
epitope is present in two positions).

This effect can be achieved in various ways, e.g. by simply
preparing fusion polypeptides comprising the structure $(CEA_e)_m$,
10 where m is an integer ≥ 2 and CEA_e is a region of constant CEA
heavy or light chain containing at least one CTL or B-cell
epitope and then introduce the modifications discussed herein
in at least one of the epitope containing sequences.

An alternative embodiment of the invention which also results
15 in the preferred presentation of multiple (e.g. at least 2)
copies of the important epitopic regions of the autologous CEA
to the immune system is the covalent coupling of the autolo-
gous CEA, subsequence or variants thereof to certain mole-
cules. For instance, polymers can be used, e.g. carbohydrates
20 such as dextran, cf. e.g. Lees A et al., 1994, Vaccine 12:
1160-1166; Lees A et al., 1990, J Immunol. 145: 3594-3600, but
also mannose and mannan are useful alternatives. Integral mem-
brane proteins from e.g. *E. coli* and other bacteria are also
useful conjugation partners. The traditional carrier molecules
25 such as keyhole limpet hemocyanin (KLH), tetanus toxoid, diph-
theria toxoid, and bovine serum albumin (BSA) are also pre-
ferred and useful conjugation partners.

Preservation of the sometimes advantageous substantial frac-
tion of B-cell epitopes or even the 3D structure of autologous
30 CEA (or domains thereof) which is subjected to modification as

described herein can be confirmed in several ways. One is sim-
ply to prepare a polyclonal antiserum directed against the
autologous CEA (e.g. an antiserum prepared in a rabbit or an-
other suitable animal) and thereafter use this antiserum as a
5 test reagent (e.g. in a competitive ELISA) against the modi-
fied proteins which are produced. Modified versions (ana-
logues) which react to the same extent with the antiserum as
does the autologous CEA must be regarded as having the same 3D
structure as the autologous CEA whereas modified CEA exhibi-
10 ting a limited (but still significant and specific) reactivity
with such an antiserum is regarded as having maintained a sub-
stantial fraction of the original B-cell epitopes.

Alternatively, a selection of monoclonal antibodies reactive
with distinct epitopes on the autologous CEA can be prepared
15 and used as a test panel. This approach has the advantage of
allowing 1) an epitope mapping of the autologous CEA and 2) a
mapping of the epitopes which are maintained in the modified
CEA prepared.

Of course, a third approach would be resolve the 3-dimensional
20 structure of the autologous CEA or of a biologically active
truncate thereof (cf. above) and compare this to the resolved
three-dimensional structure of the modified CEA prepared.
Three-dimensional structure can be resolved by the aid of X-
ray diffraction studies and NMR-spectroscopy. Further informa-
25 tion relating to the tertiary structure can to some extent be
obtained from circular dichroism studies which have the advan-
tage of merely requiring the polypeptide in pure form (whereas
X-ray diffraction requires the provision of crystallized poly-
peptide and NMR requires the provision of isotopic variants of
30 the polypeptide) in order to provide useful information about
the tertiary structure of a given molecule. However, ulti-

mately X-ray diffraction and/or NMR are necessary to obtain
conclusive data since circular dichroism can only provide in-
direct evidence of correct 3-dimensional structure via infor-
mation of secondary structure elements.

5 The present invention relies on the identification of espe-
cially well-suited regions for introduction of the foreign
element that must provide for the necessary T_H epitopes. Espe-
cially preferred regions are flexible loop regions (which do
not contribute directly to tertiary structure) as well as

10 flexible linker regions and N or C termini. Alternatively, the
introduction of the T_H epitope can be made in a region that has
a secondary structure that has a high degree of similarity
with the secondary structure of the epitope (an α-helical re-
gion may be substituted with an α-helical epitope, a β-sheet

15 region may be substituted with a β-sheet containing epitope
etc).

Especially preferred modified CEA polypeptides useful in the
present invention are selected from the group consisting of
those where the T_H epitope is introduced: in the C-terminus

20 (some variants will delete the GPI anchor as a consequence of
the omission of the native signal sequence); in the loop
structures in any one of domains 1-7 as shown in Fig. 1; and
between any two adjacent domains in CEA.

It is important to note that when a CEA construct is prepared

25 by amino acid substitution with a foreign epitope, the intro-
duction is supposed to influence minimally on the epitopes in
the relevant CEA fragment. Hence, normally a substitution will
only result in a CEA variant where the deleted CEA amino acids
constitute 30% or less of the relevant CEA (sub)sequence, and

30 under normal circumstances this number will be much lower such

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as at most 20%, at most 15%, at most 10%, and at most 7.5%.
Being a large molecule, the number can be even lower, such as
at most 5%, at most 4% and even as little as at most 3% or at
most 2%.

5 Especially preferred modified CEA polypeptides will contain
introduction of the foreign T_H epitope as an addition to the C-
or N-terminus of mature CEA (i.e. before amino acid 35 or af-
ter amino acid 681); as an insertion before any one of CEA
amino acids 1, 38, 39, 40, 41, 42, 111, 148, 149, 150, 151,
10 203, 326, 327, 328, 329, 381, 418, 419, 420, 421, 464, 504,
505, 506, 507, 559, 596, 597, 598, and 643; as a substitution
that includes deletion of any one or all of amino acids 38,
39, 40, and 41; as a substitution that includes deletion of
any or all of amino acids 148, 149, and 150; as a substitution
15 that includes deletion of any one or all of amino acids 326,
327, and 328; as a substitution that includes deletion of any
or all of amino acids 418, 419, and 420; as a substitution
that includes deletion of any or all of amino acids 504, 505,
and 506; and as a substitution that includes deletion of any
20 one or all of amino acids 596 and 597. All amino acid number-
ing corresponds to that of SEQ ID NO: 2.

Particularly preferred modified CEA polypeptides are set forth
in the sequence listing in SEQ ID NOs: 6, 8, 10, and 12, and
are also shown schematically in Fig. 2 – all these constructs
25 are made without the native CEA signal sequence and are there-
fore not membrane anchored – according to the invention it is
nevertheless intended that these 4 preferred variants (and all
other CEA variants disclosed herein) may be produced from ge-
netic material that includes this signal sequence and thereby
30 the variants become membrane anchored.

SEQ ID NO: 6 sets forth the amino acid sequence of a polypeptide that introduces the tetanus toxoid P2 and P30 epitopes in the C-terminus of CEA. The amino acid sequence in SEQ ID NO: 8 sets forth a polypeptide that introduces the P2 and P30 epi-
5 topes in the loops of domains 6 and 7, respectively. SEQ ID NO: 10 sets forth the amino acid sequence of a polypeptide that includes the P2 and P30 epitopes inserted in the linker regions between domains 4 and 5 as well as 5 and 6, respectively. Finally, SEQ ID NO: 12 sets forth the amino acid se-
10 quence of a modified CEA polypeptide where the P2 epitope is inserted in the linker between domains 4 and 5 and where P30 is substitutes domains 6 and 7.

In essence, there are at present three feasible ways of obtaining the presentation of the relevant epitopes to the im-
15 mune system: Traditional sub-unit vaccination with polypeptide antigens, administration of a genetically modified live vaccine/viral vector, and nucleic acid vaccination. These three possibilities will be discussed separately in the following:

Polypeptide vaccination

20 This entails administration to the animal in question of an immunogenically effective amount of the at least modified CEA polypeptide, e.g. as the above-discusse 1st and/or 2nd analogues. Preferably, the at least one modified CEA polypeptide is formulated together with a pharmaceutically and immunologi-
25 cally acceptable carrier and/or vehicle and, optionally an adjuvant.

When effecting presentation of the modified CEA to an animal's immune system by means of administration thereof to the animal, the formulation of the polypeptide follows the principles
30 generally acknowledged in the art.

Preparation of vaccines which contain peptide sequences as ac-
tive ingredients is generally well understood in the art, as
exemplified by US Patents 4,608,251; 4,601,903; 4,599,231;
4,599,230; 4,596,792; and 4,578,770, all incorporated herein
5   by reference. Typically, such vaccines are prepared as inject-
ables either as liquid solutions or suspensions; solid forms
suitable for solution in, or suspension in, liquid prior to
injection may also be prepared. The preparation may also be
emulsified. The active immunogenic ingredient is often mixed
10 with excipients which are pharmaceutically acceptable and com-
patible with the active ingredient. Suitable excipients are,
for example, water, saline, dextrose, glycerol, ethanol, or
the like, and combinations thereof. In addition, if desired,
the vaccine may contain minor amounts of auxiliary substances
15 such as wetting or emulsifying agents, pH buffering agents, or
adjuvants which enhance the effectiveness of the vaccines; cf.
the detailed discussion of adjuvants below.

The vaccines are conventionally administered parenterally, by
injection, for example, either subcutaneously, intracutaneous-
20 ly, or intramuscularly. Additional formulations which are
suitable for other modes of administration include supposito-
ries and, in some cases, oral, buccal, sublinqual, intrap-
eritoneal, intravaginal, anal and intracranial formulations.
For suppositories, traditional binders and carriers may in-
25 clude, for example, polyalkalene glycols or triglycerides;
such suppositories may be formed from mixtures containing the
active ingredient in the range of 0.5% to 10%, preferably 1-
2%. Oral formulations include such normally employed excipi-
ents as, for example, pharmaceutical grades of mannitol, lac-
30 tose, starch, magnesium stearate, sodium saccharine, cellu-
lose, magnesium carbonate, and the like. These compositions
take the form of solutions, suspensions, tablets, pills, cap-

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sules, sustained release formulations or powders and contain 10-95% of active ingredient, preferably 25-70%. For oral formulations, cholera toxin is an interesting formulation partner (and also a possible conjugation partner).

5   The modified CEA may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts include acid addition salts (formed with the free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic a-
10 cids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol,
15 histidine, procaine, and the like.

The vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be therapeutically effective and immunogenic. The quantity to be administered depends on the subject to be treated, including, e.g.,
20 the capacity of the individual's immune system to mount an immune response, and the degree of protection desired. Suitable dosage ranges are of the order of several hundred micrograms active ingredient per vaccination with a preferred range from about 0.1 µg to 2000 µg (even though higher amounts in the 1-
25 10 mg range are contemplated), such as in the range from about 0.5 µg to 1000 µg, preferably in the range from 1 µg to 500 µg and especially in the range from about 10 µg to 100 µg. Suitable regimens for initial administration and booster shots are also variable but are typified by an initial administration
30 followed by subsequent inoculations or other administrations.

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The manner of application may be varied widely. Any of the
conventional methods for administration of a vaccine are ap-
plicable. These include oral application on a solid physio-
logically acceptable base or in a physiologically acceptable
5   dispersion, parenterally, by injection or the like. The dosage
of the vaccine will depend on the route of administration and
will vary according to the age of the person to be vaccinated
and the formulation of the antigen.

Some of the polypeptides of the vaccine are sufficiently immu-
10 nogenic in a vaccine, but for some of the others the immune
response will be enhanced if the vaccine further comprises an
adjuvant substance. It is especially preferred to use an adju-
vant which can be demonstrated to facilitate breaking of the
autotolerance to autoantigens.

15 Various methods of achieving adjuvant effect for the vaccine
are known. General principles and methods are detailed in "The
Theory and Practical Application of Adjuvants", 1995, Duncan
E.S. Stewart-Tull (ed.), John Wiley & Sons Ltd, ISBN 0-471-
95170-6, and also in "Vaccines: New Generation Immunological
20 Adjuvants", 1995, Gregoriadis G et al. (eds.), Plenum Press,
New York, ISBN 0-306-45283-9, both of which are hereby incor-
porated by reference herein.

One group of preferred adjuvants facilitate uptake of the vac-
cine molecules by APCs, such as dendritic cells, and activate
25 these. Non-limiting examples are selected from the group con-
sisting of an immune targeting adjuvant; an immune modulating
adjuvant such as a toxin, a cytokine, and a mycobacterial de-
rivative; an oil formulation; a polymer; a micelle forming ad-
juvant; a saponin; an immunostimulating complex matrix (ISCOM
30 matrix); a particle; DDA; aluminium adjuvants; DNA adjuvants;

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γ-inulin; and an encapsulating adjuvant. In general it should
be noted that the disclosures above which relate to compounds
and agents useful as first, second and third moieties in the
modified CEA also refer *mutatis mutandis* to their use in the
5   adjuvant of a vaccine of the invention.

The application of adjuvants include use of agents such as
aluminium hydroxide or phosphate (alum), commonly used as 0.05
to 0.1 percent solution in buffered saline, admixture with
synthetic polymers of sugars (e.g. Carbopol®) used as 0.25
10 percent solution, aggregation of the protein in the vaccine by
heat treatment with temperatures ranging between 70° to 101°C
for 30 second to 2 minute periods respectively and also aggre-
gation by means of cross-linking agents are possible. Aggrega-
tion by reactivation with pepsin treated antibodies (Fab frag-
15 ments) to albumin, mixture with bacterial cells such as C.
parvum or endotoxins or lipopolysaccharide components of gram-
negative bacteria, emulsion in physiologically acceptable oil
vehicles such as mannide mono-oleate (Aracel A) or emulsion
with 20 percent solution of a perfluorocarbon (Fluosol-DA)
20 used as a block substitute may also be employed. Admixture
with oils such as squalene and IFA is also preferred.

According to the invention DDA (dimethyldioctadecylammonium
bromide) is an interesting candidate for an adjuvant as is
DNA, MF59, and γ-inulin, but also Freund's complete and incom-
25 plete adjuvants as well as quillaja saponins such as QuilA and
QS21 are interesting. Further possibilities are monophosphoryl
lipid A (MPL), and the above mentioned C3 and C3d.

Liposome formulations are also known to confer adjuvant ef-
fects, and therefore liposome adjuvants are preferred accor-
30 ding to the invention.

Also immunostimulating complex matrix type (ISCOM® matrix) ad-
juvants are preferred choices according to the invention, es-
pecially since it has been shown that this type of adjuvants
are capable of up-regulating MHC Class II expression by APCs.

5 An ISCOM® matrix consists of (optionally fractionated) sapo-
nins (triterpenoids) from Quillaja saponaria, cholesterol, and
phospholipid. When admixed with the immunogenic protein, the
resulting particulate formulation is what is known as an ISCOM
particle where the saponin constitutes 60-70% w/w, the choles-

10 terol and phospholipid 10-15% w/w, and the protein 10-15% w/w.
Details relating to composition and use of immunostimulating
complexes can e.g. be found in the above-mentioned text-books
dealing with adjuvants, but also Morein B et al., 1995, Clin.
Immunother. 3: 461-475 as well as Barr IG and Mitchell GF,

15 1996, Immunol. and Cell Biol. 74: 8-25 (both incorporated by
reference herein) provide useful instructions for the prepara-
tion of complete immunostimulating complexes.

Another highly interesting (and thus, preferred) possibility
of achieving adjuvant effect is to employ the technique de-

20 scribed in Gosselin et al., 1992 (which is hereby incorporated
by reference herein). In brief, the presentation of a relevant
antigen such as a modified CEA polypeptide of the present in-
vention can be enhanced by conjugating the antigen to antibo-
dies (or antigen binding antibody fragments) against the Fcγ

25 receptors on monocytes/macrophages. Especially conjugates be-
tween modified CEA and anti-FcγRI have been demonstrated to en-
hance immunogenicity for the purposes of vaccination.

Other possibilities involve the use of the targeting and im-
mune modulating substances (i.a. cytokines) mentioned above as

30 candidates for the first and second moieties in the modified

CEA. In this connection, also synthetic inducers of cytokines like poly I:C are possibilities.

Suitable mycobacterial derivatives are selected from the group consisting of muramyl dipeptide, complete Freund's adjuvant,
5 RIBI, and a diester of trehalose such as TDM and TDE.

Suitable immune targeting adjuvants are selected from the group consisting of CD40 ligand and CD40 antibodies or specifically binding fragments thereof (cf. the discussion above), mannose, a Fab fragment, and CTLA-4.

10 Suitable polymer adjuvants are selected from the group consisting of a carbohydrate such as dextran, PEG, starch, mannan, and mannose; a plastic polymer; and latex such as latex beads.

Yet another interesting way of modulating an immune response
15 is to include the immunogen (optionally together with adjuvants and pharmaceutically acceptable carriers and vehicles) in a "virtual lymph node" (VLN) (a proprietary medical device developed by ImmunoTherapy, Inc., 360 Lexington Avenue, New York, NY 10017-6501). The VLN (a thin tubular device) mimics
20 the structure and function of a lymph node. Insertion of a VLN under the skin creates a site of sterile inflammation with an upsurge of cytokines and chemokines. T- and B-cells as well as APCs rapidly respond to the danger signals, home to the inflamed site and accumulate inside the porous matrix of the
25 VLN. It has been shown that the necessary antigen dose required to mount an immune response to an antigen is reduced when using the VLN and that immune protection conferred by vaccination using a VLN surpassed conventional immunization using Ribi as an adjuvant. The technology is *i.a.* described
30 briefly in Gelber C *et al.*, 1998, "Elicitation of Robust Cel-

lular and Humeral Immune Responses to Small Amounts of Immuno-
gens Using a Novel Medical Device Designated the Virtual Lymph
Node", in: "From the Laboratory to the Clinic, Book of Ab-
stracts, October 12th - 15th 1998, Seascape Resort, Aptos, Cali-
5 fornia".

At any rate, for all (poly)peptide vaccine formulations ac-
cording to the invention, it is important that, if a CTL re-
sponse is aimed at, the formulation is capable of shunting the
polypeptide immunogen into the MHC type I degradation pathway
10 in order to ensure that the CTL epitopes of autologous CEA are
presented in the context of MHC Class I molecules on the sur-
face of the APC. The skilled person will know which of the
above-detailed adjuvants to choose for this specific purpose.

It is expected that the vaccine should be administered at
15 least once a year, such as at least 1, 2, 3, 4, 5, 6, and 12
times a year. More specifically, 1-12 times per year is ex-
pected, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 times
a year to an individual in need thereof. It has previously
been shown that the memory immunity induced by the use of the
20 preferred autovaccines according to the invention is not per-
manent, and therefore the immune system needs to be periodi-
cally challenged with the modified CEA.

Due to genetic variation, different individuals may react with
immune responses of varying strength to the same polypeptide.
25 Therefore, the vaccine according to the invention may comprise
several different modified CEA polypeptides in order to in-
crease the immune response, cf. also the discussion above con-
cerning the choice of foreign T-cell epitope introductions.
The vaccine may comprise two or more polypeptides, where all
30 of the polypeptides are as defined above.

The vaccine may consequently comprise 3-20 different modified polypeptides, such as 3-10 different polypeptides. However, normally the number of peptides will be sought kept to a minimum such as 1 or 2 peptides.

5 **Live vaccines**

The second alternative for effecting presentation to the immune system is the use of live vaccine technology. In live vaccination, presentation to the immune system is effected by administering, to the animal, a non-pathogenic microorganism

10 which has been transformed with a nucleic acid fragment encoding the necessary epitopic regions or a complete modified CEA polypeptide (e.g. a 1st and/or 2nd analogue). Alternatively, the microorganism is transformed with a vector incorporating such a nucleic acid fragment. The non-pathogenic microorganism can

15 be any suitable attenuated bacterial strain (attenuated by means of passaging or by means of removal of pathogenic expression products by recombinant DNA technology), e.g. *Mycobacterium bovis* BCG., non-pathogenic *Streptococcus* spp., *E. coli*, *Salmonella* spp., *Vibrio cholerae*, *Shigella*, etc. Reviews

20 dealing with preparation of state-of-the-art live vaccines can e.g. be found in Saliou P, 1995, Rev. Prat. 45: 1492-1496 and Walker PD, 1992, Vaccine 10: 977-990, both incorporated by reference herein. For details about the nucleic acid fragments and vectors used in such live vaccines, cf. the discussion be-

25 low.

Especially BCG has been used extensively as a live bacterial vaccine: The BCG vaccine has been successfully used to prevent tuberculosis around the world. Vaccination can be given after birth and results in few severe complications, even in indi-

30 viduals who are infected with human immunodeficiency virus

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type 1. BCG possesses strong immune adjuvant activity, and has
been used extensively in the treatment of superficial bladder
cancers.

As for the polypeptide vaccine, the T_H epitope and/or the first
5   and/or second and/or third moieties can, if present, be in the
form of fusion partners to the amino acid sequence derived
from the autologous CEA.

As an alternative to bacterial live vaccines, the nucleic acid
fragment of the invention discussed below can be incorporated
10 in a non-virulent viral vaccine vector. Feasible viral vectors
are selected from a pox virus such as vaccinia, MVA (modified
Vaccinia virus), canary pox, avi-pox, and chicken pox etc. Al-
ternatively, a herpes simplex virus variant can be used.

When using viral vaccines it is an interesting embodiment of
15 the invention to utilise expression vectors where the N-termi-
nal signal sequence (amino acids 1-34 in SEQ ID NO: 2) is de-
leted by omitting the nucleotides encoding it. This will have
as a result that the translation product is not exported to
the ER in the host cell, hence facilitating presentation of
20 CTL epitopes on the surface of infected cells, cf. also the
discussion under "nucleic acid vaccination".

Normally, the non-pathogenic microorganism or virus is admin-
istered only once to the animal, but in certain cases it may
be necessary to administer the microorganism more than once in
25 a lifetime.

Also, the microorganism can be transformed with nucleic
acid(s) containing regions encoding the 1st, 2nd and/or 3rd
moieties, e.g. in the form of the immunomodulating substances
described above such as the cytokines discussed as useful ad-

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juvants. A preferred version of this embodiment encompasses
having the coding region for the modified CEA and the coding
region for the immunomodulator in different open reading
frames or at least under the control of different promoters.
5 Thereby it is avoided that the modified CEA polypeptides or
epitopes are produced as fusion partners to the immunomodula-
tor. Alternatively, two distinct nucleotide fragments can be
used as transforming agents.

Nucleic acid vaccination

10 As an alternative to classic administration of a peptide-based
vaccine, the technology of nucleic acid vaccination (also
known as "nucleic acid immunisation", "genetic immunisation",
"gene immunisation" and "DNA vaccination) offers a number of
attractive features.

15 First, in contrast to the traditional vaccine approach, nu-
cleic acid vaccination does not require resource consuming
large-scale production of the immunogenic agent (e.g. in the
form of industrial scale fermentation of microorganisms pro-
ducing the modified CEA polypeptides necessary in polypeptide
20 vaccination). Furthermore, there is no need to device purifi-
cation and refolding schemes for the immunogen. And finally,
since nucleic acid vaccination relies on the biochemical appa-
ratus of the vaccinated individual in order to produce the ex-
pression product of the nucleic acid introduced, the optimum
25 posttranslational processing of the expression product is ex-
pected to occur; this is especially important in the case of
autovaccination, since, as mentioned above, a significant
fraction of the original B-cell epitopes should be preserved
in the modified CEA polypeptides derived from extracellularly
30 exposed polypeptide sequences, and since B-cell epitopes in

principle can be constituted by parts of any (bio)molecule
(e.g. carbohydrate, lipid, protein etc.). Therefore, native
glycosylation and lipidation patterns of the immunogen may
very well be of importance for the overall immunogenicity and
5 this is best ensured by having the host producing the immuno-
gen.

Two further features render nucleic acid vaccination espe-
cially interesting in the context of the present invention. By
using DNA as a vaccine agent, it is relatively uncomplicated
10 to ensure presentation of CTL epitopes in the MHC class I con-
text on the APCs (as long as translocation signals directing
the translation product to the ER are omitted). Further, it
has been repeatedly demonstrated that immunizations including
administration of DNA leads to a shift in T helper cell pro-
15 file from Th2 to Th1 cells, and since the adverse allergic re-
actions mediated by CEA are first and foremost supported by
Th2 cells, the use of DNA vaccination will in itself provide a
beneficial effect on the underlying disease.

Hence, an important embodiment of the method of the invention
20 involves that presentation is effected by administering a nu-
cleic acid fragment encoding a modified CEA polypeptide. Pre-
ferably, this is done by using a nucleic acid fragment which
encodes and expresses the above-discussed first analogue. If
the first analogue is equipped with the above-detailed T_H epi-
25 topes and/or first and/or second and/or third moieties, these
are then present in the form of fusion partners to the amino
acid sequence derived from the autologous CEA, the fusion con-
struct being encoded by the nucleic acid fragment.

As for the traditional vaccination approach, the nucleic acid
30 vaccination can be combined with *in vivo* introduction, into

the APC, of at least one nucleic acid fragment encoding and
expressing the second analogue. The considerations pertaining
to 1st, 2nd and 3rd moieties and T_H epitopes apply also here.

In this embodiment, the introduced nucleic acid is preferably
5 DNA which can be in the form of naked DNA, DNA formulated with
charged or uncharged lipids, DNA formulated in liposomes,
emulsified DNA, DNA included in a viral vector, DNA formulated
with a transfection-facilitating protein or polypeptide, DNA
formulated with a targeting protein or polypeptide, DNA formu-
10 lated with Calcium precipitating agents, DNA coupled to an in-
ert carrier molecule, and DNA formulated with an adjuvant. In
this context it is noted that practically all considerations
pertaining to the use of adjuvants in traditional vaccine for-
mulation apply for the formulation of DNA vaccines. Hence, all
15 disclosures herein which relate to use of adjuvants in the
context of polypeptide based vaccines apply mutatis mutandis
to their use in nucleic acid vaccination technology. The same
holds true for other considerations relating to formulation
and mode and route of administration and, hence, also these
20 considerations discussed above in connection with a tradi-
tional vaccine apply mutatis mutandis to their use in nucleic
acid vaccination technology.

One especially preferred type of formulation of nucleic acid
vaccines are microparticles containing the DNA. Suitable mi-
25 croparticles are e.g. described in WO 98/31398.

Furthermore, the nucleic acid(s) used as an immunization agent
can contain regions encoding the 1st, 2nd and/or 3rd moieties,
e.g. in the form of the immunomodulating substances described
above such as the cytokines discussed as useful adjuvants. A
30 preferred version of this embodiment encompasses having the

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coding region for the modified CEA and the coding region for
the immunomodulator in different open reading frames or at
least under the control of different promoters. Thereby it is
avoided that the modified CEA is produced as a fusion partner
5 to the immunomodulator. Alternatively, two distinct nucleotide
fragments can be used, but this is less preferred because of
the advantage of ensured co-expression when having both coding
regions included in the same molecule.

Under normal circumstances, the nucleic acid of the vaccine is
10 introduced in the form of a vector wherein expression is under
control of a viral promoter. For more detailed discussions of
vectors according to the invention, cf. the discussion below.
Also, detailed disclosures relating to the formulation and use
of nucleic acid vaccines are available, cf. Donnelly JJ et al,
15 1997, Annu. Rev. Immunol. 15: 617-648 and Donnelly JJ et al.,
1997, Life Sciences 60: 163-172. Both of these references are
incorporated by reference herein.

The expression cassette in the nucleic acid vaccine can be
constructed so as to ensure that no export of the expression
20 product takes place (e.g. by omitting signal sequences that
would result in membrane integration or secretion). In this
way, only minute amounts of expression product will be ex-
ported, whereas the remainder will be processed and presented
as peptide fragments in the context of MHC molecules.

25 Hence, when using nucleic acid vaccines it is an interesting
embodiment of the invention to utilise expression vectors
where the N-terminal CEA signal sequence (amino acids 1-34 in
SEQ ID NO: 2) is deleted by omitting the nucleotides encoding
it. This will have as a result that the translation product is
30 not exported to the ER in the host cell, hence facilitating

presentation of CTL epitopes on the surface of infected cells. In this way, only minute amounts of expression product will be exported, whereas the remainder will be processed and presented as peptide fragments in the context of MHC molecules.

5 Hence, no or only a very limited antibody response will be induced, whereas a CTL response will be mounted.

Combination of approaches

As discussed above under the "Background of the Invention", various prime-boost strategies have proven effective in faci-
10 litating an improved immune response. Hence, according to the present invention, use of any combination of nucleic acid vaccination, live vaccination and polypeptide vaccination may be utilised. However, it is especially preferred to prime via nucleic acid or viral vaccination and boost with a polypeptide
15 vaccine, preferably where the polypeptide vaccine contains the expression product fromt the nucleic acid of the priming vaccine.

Polypeptides of the invention

All modified CEA polypeptides discussed in the above disclo-
20 sure of the method of the invention are believed to be inventive in their own right. Hence the invention also relates to modified human CEA polypeptide that is capable of inducing an immune response against autologous CEA in a human subject, the, which comprises at least about 80 CEA-derived amino a-
25 cids, either in the form of at least about 80 consecutive CEA-derived amino acids or in the form of at least about 80 amino acids constituted of uninterrupted CEA-derived CTL epitopes, and at least one first non-human T helper epitope (T_H epitope).

All teaching set forth above concerning possible embodiments
of the modified CEA also applies *mutatis mutandis* to the part
of the invention that relates to modified CEA as such. Hence,
each and every embodiment of modified CEA described in context
5 of the method of the invention also applies to embodiments of
modified CEA as such.

It should be noted that preferred modified CEA polypeptides of
the invention (and also the relevant modified CEA polypeptides
used in the methods of the invention) comprise modifications
10 which results in a polypeptide having a sequence identity of
at least 70% with the autologous CEA or with a subsequence
thereof of at least 10 amino acids in length. Higher sequence
identities are preferred, e.g. at least 75% or even at least
80% or 85%. The sequence identity for proteins and nucleic a-
15 cids can be calculated as $(N_{ref}-N_{dif}) \cdot 100/N_{ref}$, wherein N_{dif} is
the total number of non-identical residues in the two se-
quences when aligned and wherein N_{ref} is the number of residues
in one of the sequences. Hence, the DNA sequence AGTCAGTC will
have a sequence identity of 75% with the sequence AATCAATC
20 (N_{dif}=2 and N_{ref}=8).

Nucleic acid fragments and vectors of the invention

It will be appreciated from the above disclosure that the
modified polypeptides can be prepared by means of recombinant
gene technology but also by means of chemical synthesis or
25 semisynthesis; the latter two options are especially relevant
when the modification consists in coupling to protein carriers
(such as KLH, diphtheria toxoid, tetanus toxoid, and BSA) and
non-proteinaceous molecules such as carbohydrate polymers and
of course also when the modification comprises addition of

side chains or side groups to an polypeptide-derived peptide
chain.

For the purpose of recombinant gene technology, and of course
also for the purpose of nucleic acid immunization, nucleic

5   acid fragments encoding the necessary modified CEA polypep-
tides are important chemical products. Hence, an important
part of the invention pertains to a nucleic acid fragment
which encodes a modified CEA polypeptide described above,
preferably a polypeptide wherein has been introduced a foreign

10 T_H-cell epitope by means of insertion and/or addition, prefera-
bly by means of substitution and/or deletion. The nucleic acid
fragments of the invention are either DNA or RNA fragments.

The nucleic acid fragments of the invention will normally be
inserted in suitable vectors to form cloning or expression

15 vectors carrying the nucleic acid fragments of the invention;
such novel vectors are also part of the invention. Details
concerning the construction of these vectors of the invention
will be discussed in context of transformed cells and microor-
ganisms below. The vectors can, depending on purpose and type

20 of application, be in the form of plasmids, phages, cosmids,
mini-chromosomes, or virus, but also naked DNA which is only
expressed transiently in certain cells is an important vector.
Preferred cloning and expression vectors of the invention are
capable of autonomous replication, thereby enabling high copy-

25 numbers for the purposes of high-level expression or high-
level replication for subsequent cloning.

The general outline of a vector of the invention comprises the
following features in the 5'→3' direction and in operable
linkage: a promoter for driving expression of the nucleic acid

30 fragment of the invention, optionally a nucleic acid sequence

encoding a leader peptide enabling secretion of or integration
into the membrane of the polypeptide fragment, the nucleic
acid fragment of the invention, and a nucleic acid sequence
encoding a terminator. When operating with expression vectors
5 in producer strains or cell-lines it is for the purposes of
genetic stability of the transformed cell preferred that the
vector when introduced into a host cell is integrated in the
host cell genome. In contrast, when working with vectors to be
used for effecting *in vivo* expression in an animal (i.e. when
10 using the vector in DNA vaccination) it is for security rea-
sons preferred that the vector is not capable of being inte-
grated in the host cell genome; typically, naked DNA or non-
integrating viral vectors are used, the choices of which are
well-known to the person skilled in the art.

15 The vectors of the invention are used to transform host cells
to produce the modified CEA of the invention. Such transformed
cells, which are also part of the invention, can be cultured
cells or cell lines used for propagation of the nucleic acid
fragments and vectors of the invention, or used for recombi-
20 nant production of the modified CEA of the invention. Alterna-
tively, the transformed cells can be suitable live vaccine
strains wherein the nucleic acid fragment (one single or mul-
tiple copies) have been inserted so as to effect secretion or
integration into the bacterial membrane or cell-wall of the
25 modified CEA.

Preferred transformed cells of the invention are microorga-
nisms such as bacteria (such as the species Escherichia [e.g.
E. coli], Bacillus [e.g. Bacillus subtilis], Salmonella, or
Mycobacterium [preferably non-pathogenic, e.g. M. bovis BCG]),
30 yeasts (such as Saccharomyces cerevisiae), and protozoans. Al-
ternatively, the transformed cells are derived from a multi-

cellular organism such as a fungus, an insect cell, a plant
cell, or a mammalian cell. Most preferred are cells derived
from a human being, cf. the discussion of cell lines and vec-
tors below.

5   For the purposes of cloning and/or optimised expression it is
preferred that the transformed cell is capable of replicating
the nucleic acid fragment of the invention. Cells expressing
the nucleic fragment are preferred useful embodiments of the
invention; they can be used for small-scale or large-scale
10 preparation of the modified CEA or, in the case of non-patho-
genic bacteria, as vaccine constituents in a live vaccine.

When producing the modified CEA of the invention by means of
transformed cells, it is convenient, although far from essen-
tial, that the expression product is either exported out into
15 the culture medium or carried on the surface of the trans-
formed cell.

When an effective producer cell has been identified it is pre-
ferred, on the basis thereof, to establish a stable cell line
which carries the vector of the invention and which expresses
20 the nucleic acid fragment encoding the modified CEA. Prefera-
bly, this stable cell line secretes or carries the modified
CEA of the invention, thereby facilitating purification
thereof.

In general, plasmid vectors containing replicon and control
25 sequences which are derived from species compatible with the
host cell are used in connection with the hosts. The vector
ordinarily carries a replication site, as well as marking se-
quences which are capable of providing phenotypic selection in
transformed cells. For example, *E. coli* is typically trans-
30 formed using pBR322, a plasmid derived from an *E. coli* species

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(see, e.g., Bolivar et al., 1977). The pBR322 plasmid contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR plasmid, or other microbial plasmid or phage must also con-
5 tain, or be modified to contain, promoters which can be used by the prokaryotic microorganism for expression.

Those promoters most commonly used in recombinant DNA construction include the B-lactamase (penicillinase) and lactose promoter systems (Chang et al., 1978; Itakura et al., 1977;
10 Goeddel et al., 1979) and a tryptophan (trp) promoter system (Goeddel et al., 1979; EP-A-0 036 776). While these are the most commonly used, other microbial promoters have been discovered and utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to
15 ligate them functionally with plasmid vectors (Siebwenlist et al., 1980). Certain genes from prokaryotes may be expressed efficiently in *E. coli* from their own promoter sequences, precluding the need for addition of another promoter by artificial means.

20 In addition to prokaryotes, eukaryotic microbes, such as yeast cultures may also be used, and here the promoter should be capable of driving expression. *Saccharomyces cerevisiase*, or common baker's yeast is the most commonly used among eukaryotic microorganisms, although a number of other strains are
25 commonly available such as *Pichia pastoris*. For expression in *Saccharomyces*, the plasmid YRp7, for example, is commonly used (Stinchcomb et al., 1979; Kingsman et al., 1979; Tschemper et al., 1980). This plasmid already contains the trpl gene which provides a selection marker for a mutant strain of yeast lack-
30 ing the ability to grow in tryptophan for example ATCC No. 44076 or PEP4-1 (Jones, 1977). The presence of the trpl lesion

as a characteristic of the yeast host cell genome then pro-
vides an effective environment for detecting transformation by
growth in the absence of tryptophan.

Suitable promoting sequences in yeast vectors include the pro-
5 moters for 3-phosphoglycerate kinase (Hitzman et al., 1980) or
other glycolytic enzymes (Hess et al., 1968; Holland et al.,
1978), such as enolase, glyceraldehyde-3-phosphate dehydro-
genase, hexokinase, pyruvate decarboxylase, phosphofructokina-
se, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase,
10 pyruvate kinase, triosephosphate isomerase, phosphoglucose
isomerase, and glucokinase. In constructing suitable expres-
sion plasmids, the termination sequences associated with these
genes are also ligated into the expression vector 3' of the
sequence desired to be expressed to provide polyadenylation of
15 the mRNA and termination.

Other promoters, which have the additional advantage of tran-
scription controlled by growth conditions are the promoter re-
gion for alcohol dehydrogenase 2, isocytochrome C, acid phos-
phatase, degradative enzymes associated with nitrogen metabo-
20 lism, and the aforementioned glyceraldehyde-3-phosphate dehy-
drogenase, and enzymes responsible for maltose and galactose
utilization. Any plasmid vector containing a yeast-compatible
promoter, origin of replication and termination sequences is
suitable.

25 In addition to microorganisms, cultures of cells derived from
multicellular organisms may also be used as hosts. In princi-
ple, any such cell culture is workable, whether from verte-
brate or invertebrate culture. However, interest has been
greatest in vertebrate cells, and propagation of vertebrate in
30 culture (tissue culture) has become a routine procedure in re-

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cent years (Tissue Culture, 1973). Examples of such useful
host cell lines are VERO and HeLa cells, Chinese hamster ovary
(CHO) cell lines, and W138, BHK, COS-7 293 and MDCK cell
lines.

5 Expression vectors for such cells ordinarily include (if nec-
essary) an origin of replication, a promoter located in front
of the gene to be expressed, along with any necessary ribosome
binding sites, RNA splice sites, polyadenylation site, and
transcriptional terminator sequences.

10 For use in mammalian cells, the control functions on the ex-
pression vectors are often provided by viral material. For ex-
ample, commonly used promoters are derived from polyoma, Ade-
novirus 2, and most frequently Simian Virus 40 (SV40). The
early and late promoters of SV40 virus are particularly useful
15 because both are obtained easily from the virus as a fragment
which also contains the SV40 viral origin of replication (Fi-
ers et al., 1978). Smaller or larger SV40 fragments may also
be used, provided there is included the approximately 250 bp
sequence extending from the *Hind*III site toward the *Bgl*I site
20 located in the viral origin of replication. Further, it is
also possible, and often desirable, to utilize promoter or
control sequences normally associated with the desired gene
sequence, provided such control sequences are compatible with
the host cell systems.

25 An origin of replication may be provided either by construc-
tion of the vector to include an exogenous origin, such as may
be derived from SV40 or other viral (e.g., Polyoma, Adeno,
VSV, BPV) or may be provided by the host cell chromosomal re-
plication mechanism. If the vector is integrated into the host
30 cell chromosome, the latter is often sufficient.

Compositions of the invention

The invention also relates to an immunogenic composition which comprises, as an effective immunogenic agent at least one of the modified CEA polypeptides described herein in admixture
5 with a pharmaceutically and immunologically acceptable carrier, vehicle, diluent, or excipient, and optionally an adjuvant, cf. also the discussion of these entities in the description of the method of the invention above.

Furthermore, the invention also relates to a composition for
10 inducing production of antibodies autologous CEA, the composition comprising

- a nucleic acid fragment or a vector of the invention, and

- a pharmaceutically and immunologically acceptable diluent and/or vehicle and/or carrier and/or excipient and/or ad-
15   juvant.

Formulation and other specifics concerning such compositions are discussed in the relevant section regarding nucleic acid immunisation above.

In the following examples we present a discussion of the pre-
20 ferred constructs of the invention as well as of their preparation and the testing of the immunological properties of these constructs.

EXAMPLES

CEA DNA constructions.

Modified CEA constructs are designed and constructed as gener-
ally and specifically described above utilising standard pro-
5 tocols known in the art.

For use as DNA vaccines, the DNA encoding modified CEA can
thereafter be directly cloned into suitable, commercially
available DNA vaccination vectors such as pcDNA, pHP, pCI etc.

Expression and purification of CEA proteins

10 A variety of expression systems could be employed in order to
generate recombinant modified CEA polyptides. This includes
expression systems based on e.g. bacterial, insect cells,
yeast and mammalian cells. In either system, stable lines
and/or clones will be established and grown in suitable vo-
15 lumes for protein production. Various protein purification
methods (e.g. precipitations and chromatographic methods such
as gel filtrations, affinity chromatography, ion exchange
chromatography, HPLC etc.) can be used to purify CEA proteins.
If necessary, refolding procedures may be also applied to
20 yield products suitable for vaccinations.

DNA and protein vaccinations

The modified CEA polypeptide or nucleic acid expression vector
is injected into a suitable animal species such as mouse, rat,
guinea pig, rabbit, or monkey.

25 In case of CEA nucleic acid vaccines, the animals are usually
immunized a total of 3-6 times, for example at weeks 0, 2, 4,

6 and 8. The DNA vaccines can either consist of plasmid DNA
dissolved in water, saline or a suitable buffer such as tris-
based buffers, PBS etc – or the DNA can be formulated in a
suitable delivery system such as microparticles and liposomes,
5   cf. the discussion pertaining to formulations above.

In case of protein-based CEA vaccines, the purified recombi-
nant modified CEA proteins can be mixed with a suitable adju-
vant such as for example Freund's Adjuvant, ISA-51, aluminum-
based adjuvants (aluminium phosphate or aluminium hydroxide,
10 e.g. from Danfoss), Calcium Phosphate, QS21 (Antigenics), MF59
(Chiron Corp.), and Ribi (Glaxo SmithKline). Protein vaccines
are usually administered 3-5 times, for example at weeks 0, 3,
6, 9, 12.

CEA nucleic acid vaccines and CEA protein vaccines can also be
15 combined in any vaccination scheme in a prime-boost strategy.
An example of such a vaccination scheme could be one initial
immunisation with a CEA DNA expression vector at week 0 and
subsequent booster injections with modified CEA protein at
weeks 3, 6 and 9 – however, any other combination of DNA and
20 protein vaccinations could be used.

Antibody titer determination

Sera from vaccinated animals can be tested for CEA specific
antibodies by ELISA. 96-well Maxisorb plates (e.g obtained
from Nunc, Life Technologies, Taastrup, Denmark) can be coated
25 with a suitable volume (e.g. 50 ul) of CEA protein in a suit-
able buffer such as carbonate buffer pH 9.6 in a suitable con-
centration giving a final CEA content of e.g. 1 ug/well. The
plates are incubated, e.g. for 1 hour, washed in washing
buffer, e.g. PBS + 0.5M NaCl + 1% Triton X-100 and then
30 blocked for e.g. 1 hour in dilution buffer that could e.g. be

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washing buffer plus 1% BSA. Standards and diluted serum sam-
ples can be added in duplicate and incubated in the plates,
e.g. for 30 minutes. After washing, a dilution of secondary
antibody (e.g. HRP conjugated rabbit-anti-mouse IgG e.g. from
5 DAKO, Glostrup, Denmark) can be added (e.g diluted 1:1000 in
dilution buffer) and incubated for 30 minutes. The plates can
then be washed in washing buffer, and a chromogenic substrate,
e.g. OPD substrate (e.g. from Sigma-Aldrich, Vallensbæk
Strand, Denmark) can be added. The reaction can be stopped
10 with e.g 2N H_2SO_4 and the optical density be measured in e.g. a
Dynex MRX ELISA plate reader at 490nm. Serum antibody concen-
trations can be calculated e.g. by relating the optical densi-
ties of the samples to a standard curve. In order to generate
the standard curve, a wide range of anti-CEA antibodies are
15 available commercially and/or from academic sources.

The ELISA can be modified for different purposes, e.g. the re-
activity against CEA peptides can be monitored using peptide
ELISA for mapping of the fine specificity of anti-CEA anti-
sera. Sandwich ELISA can be used to monitor whether the anti-
20 CEA antisera contains reactivities that can displace e.g. a
biotin-labeled, therapeutically relevant anti-CEA antibody
from binding to plate-coated CEA. Specialized ELISA kits can
be used to determine the isotype subclass distribution in
anti-CEA etc.

25 *Assays to monitor anti-CEA CTL activity*

It can be investigated whether immunization with CEA vaccines
(DNA and/or protein-based vaccines) can induce a CEA-specific
CTL response. CEA derived peptides (e.g. YLSGANLNL, YLSGADLNL,
HLFGYSWYK, SYLSGANLNL, QYSWFVNGTF, TYACFVSNL) that are known
30 to be able to bind to MHC class I can be synthesized and used

to pulse antigen presenting cells in e.g. typical cytotoxic T cell assays. CEA expressing target cells (e.g. MHC class I expressing tumor cell lines transfected with CEA) can be used as targets for CEA-specific cytotoxic T lymphocytes (CTLs).

5 Mice will be vaccinated with CEA-encoding DNA in vivo expression vectors and/or proteins using an appropriate vaccination scheme, cf. above. As positive control, mice could be immunized with e.g. MHC class I peptides derived from the CEA sequence. After a suitable time interval, e.g. three weeks after

10 the first immunization, splenocytes from immunized mice can be re-stimulated e.g. with mytomicin C-treated (e.g. 50 µg/ml, 20 min at 37 °C) syngeneic splenocytes loaded with CEA peptides. For this re-stimulation process, a suitable number (e.g. 100×10^6) of peptide-loaded syngeneic splenocytes can be mixed

15 with a suitable number (e.g. 60×10^6) of splenocytes from vaccinated mice in and incubated at 37 °C for e.g. 7 days. After the restimulation process, the cytotoxic activity of the effector cells can be monitored e.g. in a chromium release assay. A suitable number (e.g. 5×10^6) of target cells is labeled

20 with ^{51}Chromium (e.g. 200 mCi), if necessary loaded with CEA-derived peptide, and used as targets in a ^{51}Chromium release assay. Cell lines transfected with human CEA can also be used as targets for CTLs. Such CTL assays can e.g. be performed in normal wild type mice, human CEA transgenic mice and/or mice

25 transgenic for human HLA class I molecules (e.g. HHD mice) using suitable compatible target cells and cells for restimulation.

The ability of a CEA vaccine to induce CEA-specific CTL responses can also be measured using other assay methods inclu-

30 ding CEA specific tetramer stainings and Elispot assays; all such methods are well-known to the person skilled in immunology.

CEA tumor models

To test the effect of CEA vaccination in tumor models, trans-
genic mice expressing human CEA or normal strains such as e.g.
Balb/c, C57Bl/6 or others could be obtained either from a com-
5   mercial animal supplier or an academic or other collaborator.
A transplantable tumor cell line expressing the CEA antigen
can be used to create an animal model that can be used to
monitor whether CEA vaccination can inhibit a CEA positive tu-
mor challenge. The transplantable tumor cell line can either
10 be a tumor cell line which is compatible with the mouse strain
transfected with the human CEA sequence – or it can be a tumor
cell line derived from a tumor dissected from CEA transgenic
mice. The tumor model studies can be designed either as pre-
vention or as treatment studies. In prevention studies, the
15 mice are implanted with CEA expressing tumours after the
course of immunization and the growth of the tumour is meas-
ured in a designated period. In treatment studies, mice are
implanted with the CEA expressing tumours followed by single
or multiple vaccinations with the CEA vaccines. Tumour growth
20 can then be followed for a designated period.

One suitable such animal model is described in Eades-Perner AM
et al. 1994, Cancer Res **54**, 4169-4176.

Passive transfer of anti-CEA antibodies

In order to determine whether antibodies induced by CEA vacci-
25 nations can inhibit growth of CEA expressing tumors, a passive
transfer model can be used. Sera from mice vaccinated with mo-
dified CEA protein and/or DNA can be pooled and the CEA spe-
cific antibody concentration determined by ELISA. A suitable
volume (e.g. 100 to 200 µl) of the pooled mouse serum can be

injected into the peritoneum of naïve mice one day before sub-
cutaneous challenge with a suitable number of CEA expressing
tumor cells. The tumor cells can either be obtained from a
commercial source or tumor cells transfected with the human
5 CEA sequence. Control animals will be injected with non-spe-
cific mouse IgG (e.g. from Jackson ImmunoResearch Laborato-
ries, Inc., West Grove, PA) or with serum from mice injected
with an irrelevant antigen or adjuvant only. The mice can be
immune deficient strains, e.g. nude mice or SCID mice, allow-
10 ing transplantation with MHC incompatible tumor cell lines,
e.g. human tumor cell lines expressing CEA. Tumour growth will
then be monitored for a suitable time period, e.g. several
weeks. Similar studies can be performed where the animal spe-
cies which is immunized with CEA vaccines are not mice (e.g.
15 rats or rabbits), and the protocol is adjusted accordingly.

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CLAIMS

1. A method for inducing an immune response against autologous carcinoembryonic antigen (CEA) in an animal, including a human being, the method comprising effecting uptake and processing by antigen presenting cells (APCs) in the animal of at least one modified CEA polypeptide or of a nucleic acid encoding the modified CEA polypeptide or of a pharmaceutically acceptable microorganism or virus expressing the modified CEA polypeptide, said at least one modified CEA polypeptide comprising

- at least about 80 CEA-derived amino acids, either in the form of at least about 80 consecutive CEA-derived amino acids or in the form of at least about 80 amino acids constituted of uninterrupted CEA-derived CTL epitopes, and

- at least one first T helper epitope (T_H epitope) foreign to the animal,

thereby inducing a CTL response and/or an antibody response that targets the autologous CEA.

2. The method according to claim 1, wherein the Modified CEA polypeptide comprises at least about 100 CEA derived amino a-cids, such as at least about 120, 140, 160 or 180 amino acids, preferably at least about 200, such as at least about 220, 250, 300, 400, or 500 amino acids.

3. The method according to claim 1 or 2, wherein at least one CEA-derived CTL epitope is presented by the APC in association with an MHC Class I molecule on the surface of the APC and/or wherein said at least one first foreign T_H epitope is presented

by an APC in association with an MHC Class II molecule on the surface of the APC.

4. The method according to any one of the preceding claims, wherein the APC is a dendritic cell or a macrophage.

5. 5. The method according to any one of the preceding claims, wherein at least one modified CEA polypeptide is in the form of one first analogue of CEA, said first analogue comprising a variation of the amino acid sequence of CEA, said variation containing CEA-derived CTL epitope(s) and the at least one

10. first foreign T_H epitope.

6. The method according to claim 5, wherein the at least one first analogue contains a substantial fraction of known and predicted CTL epitopes from autologous CEA.

7. The method according to claim 6, wherein the substantial

15. fraction of known and predicted CTL epitopes in the amino acid sequence of the analogue are recognized by at least 90% of the MHC-I haplotypes recognizing all known and predicted CTL epitopes in CEA.

8. The method according to any one of claims 5-7, wherein sub-

20. stantially all known CTL epitopes of the autologous CEA are present in the first analogue and/or wherein substantially all predicted CTL epitopes of the autologous CEA are present in the at least first analogue.

9. The method according to any one of claims 5-8, wherein the

25. at least one first analogue further comprises at least one B-cell epitope of the autologous CEA, so that immunization of the animal with the first analogue induces production of antibodies in the animal against the autologous CEA.

10. The method according to any one of the preceding claims, wherein one modified CEA polypeptide is in the form of at least one second analogue of the autologous CEA, said second analogue containing at least one B-cell epitope of the autolo-
5 gous CEA, so that immunization of the animal with the second analogue induces production of antibodies against the autologous CEA.

11. The method according to claim 10, wherein at least one second foreign T_H epitope is included in the second analogue.

10 12. The method according to any one of claims 6-11, wherein the first and/or second analogue(s) comprise(s) a substantial fraction of the B-cell epitopes of the autologous CEA.

13. The method according to any one of the preceding claims, wherein the modified CEA polypeptide substantially includes
15 the amino acid sequence of at least one domain, such as at least 2, 3, 4, 5, 6 or all 7 domains of CEA.

14. The method according to any one of the preceding claims, wherein the modified CEA polypeptide can be provided by sub-jecting CEA to amino acid substitution and/or deletion and/or
20 insertion and/or addition.

15. The method according to any one of the preceding claims, wherein the modified CEA polypeptide comprises

   - at least one first moiety effecting targeting of the modified CEA polypeptide to an antigen presenting cell
25   (APC), and/or

   - at least one second moiety stimulating the immune system, and/or

- at least one third moiety optimising presentation of the
modified CEA to the immune system.

16. The method according to any one of the preceding claims,
wherein the modified CEA polypeptide includes duplication of
5 at least one B-cell epitope or of at least one CTL epitope of
the autologous CEA.

17. The method according to any one of the preceding claims,
wherein the first and/or, where applicable, second foreign T_H
epitope(s) is/are immunodominant and/or wherein the first
10 and/or, where applicable, second foreign T_H epitope(s) is/are
promiscuous.

18. The method according to any one of the preceding claims,
wherein the modified CEA polypeptide is provided by introduc-
tion of a foreign T_H epitope that is introduced in any one of
15 the following regions of CEA:

- in the C-terminus,

- in the N-terminus,

- in the loop structures in any one of domains 1-7 as shown
in Fig. 1, and

20   - between any two adjacent domains of CEA.

19. The method according to claim 18, wherein the foreign T_H
epitope is introduced

- as an addition to the C- or N-terminus of mature CEA;

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- as an insertion before any one of CEA amino acids 1, 38, 39, 40, 41, 42, 111, 148, 149, 150, 151, 203, 326, 327, 328, 329, 381, 418, 419, 420, 421, 464, 504, 505, 506, 507, 559, 596, 597, 598, and 643;

5
- as a substitution that includes deletion of any one or all of amino acids 38, 39, 40, and 41;

- as a substitution that includes deletion of any or all of amino acids 148, 149, and 150;

- as a substitution that includes deletion of any one or
10   all of amino acids 326, 327, and 328;

- as a substitution that includes deletion of any or all of amino acids 418, 419, and 420;

- as a substitution that includes deletion of any or all of amino acis 504, 505, and 506; and

15
- as a substitution that includes deletion of any one or all of amino acids 596 and 597,

wherein the amino acid numbering corresponds to that of SEQ ID NO: 2.

20. The method according to any one of the preceding claims
20 wherein the C-terminal GPI-anchor of CEA is preserved in the modified CEA polypeptide.

21. The method according to any one of claims 1-19, wherein the C-terminal GPI-anchor of CEA is removed.

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22. The method according to any one of claims 11-19, wherein foreign T_H epitope(s) is/are selected from a natural T_H epitope and an artificial MHC-II binding peptide sequence

23. The method according to claim 22, wherein the natural T-
5 cell epitope is selected from a Tetanus toxoid epitope, a diphtheria toxoid epitope, an influenza virus hemagluttinin epitope, and a *P. falciparum* CS epitope.

24. The method according to any one the preceding claims, wherein non-CEA derived components such as foreign T_H epitopes
10 or first, second and third moieties as defined in claim 15 are present in the form of

   - side groups attached covalently or non-covalently to suitable chemical groups in the amino acid sequence of the autologous CEA or a subsequence thereof, and/or

15   - fusion partners to the amino acid sequence derived from the autologous CEA.

25. The method according to claim 24, wherein

   - the first moiety is a substantially specific binding partner for an APC specific surface antigen such as a
20   carbohydrate for which there is a receptor on the APC, e.g. mannan or mannose, or wherein the first moiety is a hapten,

   - the second moiety is a cytokine selected from interferon γ (IFN-γ), Flt3L, interleukin 1 (IL-1), interleukin 2 (IL-
25   2), interleukin 4 (IL-4), interleukin 6 (IL-6), inter- leukin 12 (IL-12), interleukin 13 (IL-13), interleukin 15 (IL-15), and granulocyte-macrophage colony stimulating

factor (GM-CSF), or an effective part thereof; a heat-
shock protein selected from heat shock protein 70
(HSP70), heat shock protein 90 (HSP90), heat shock cog-
nate 70 (HSC70), glucose-regulated protein 94 (GRP94),
5   and calreticulin (CRT), or an effective part thereof; or
a hormone,

- the third moiety is a lipid such as a palmitoyl group, a
myristyl group, a farnesyl group, a geranyl-geranyl
group, a GPI-anchor, and an N-acyl diglyceride group.

10 26. The method according to claim any one the preceding
claims, wherein the modified CEA polypeptide substantially
preserves the 3-dimensional structure of at least one of CEA
domains 1-7.

27. The method according to claim 26, wherein the 3-dimen-
15 sional structures of at least 4 of CEA domains 1-7 is substan-
tially preserved, preferably those of domains 1-4.

28. The method according to claim 27, wherein the 3-dimen-
sional structures of all CEA domains are substantially pre-
served.

20 29. The method according to any one of the preceding claims,
comprising administering, to the animal, an immunogenically
effective amount of the at least one modified CEA polypeptide.

30. The method according to claim 29, wherein said modified
CEA is formulated together with a pharmaceutically and immu-
25 nologically acceptable carrier and/or vehicle and, optionally
an adjuvant.

31. The method according to claim 30, wherein the adjuvant is
selected from the group consisting of an immune targeting ad-
juvant; an immune modulating adjuvant such as a toxin, a cyto-
kine, and a mycobacterial derivative; an oil formulation; a
5 polymer; a micelle forming adjuvant; a saponin; an immu-
nostimulating complex matrix (ISCOM matrix); a particle; DDA;
aluminium adjuvants; DNA adjuvants; γ-inulin; and an encapsu-
lating adjuvant.

32. The method according to claim 31, wherein the cytokine is
10 as defined as in claim 25, or an effective part thereof,
wherein the toxin is selected from the group consisting of
listeriolycin (LLO), Lipid A (MPL, L180.5/RalLPS), and heat-
labile enterotoxin, wherein the mycobacterial derivative is
selected from the group consisting of muramyl dipeptide, com-
15 plete Freund's adjuvant, RIBI, and a diester of trehalose such
as TDM and TDE, wherein the immune targeting adjuvant is se-
lected from the group consisting of CD40 ligand, CD40 antibo-
dies or specifically binding fragments thereof, mannose, a Fab
fragment, and CTLA-4, wherein the oil formulation comprises
20 squalene or incomplete Freund's adjuvant, wherein the polymer
is selected from the group consisting of a carbohydrate such
as dextran, PEG, starch, mannan, and mannose; a plastic poly-
mer; and latex such as latex beads, wherein the saponin is
Quillaja saponaria saponin, Quil A, and QS21, and wherein the
25 particle comprises latex or dextran.

33. The method according to any one of claims 29-32, which in-
cludes administration via a route selected from the oral route
and the parenteral route such as the intracutaneous, the sub-
cutaneous, the peritoneal, the buccal, the sublinqual, the
30 epidural, the spinal, the anal, and the intracranial routes.

34. The method according to any of claim 29-33, which includes at least one administration a year, such as at least 2, 3, 4, 5, 6, and 12 administrations a year.

35. The method according to any one of claims 1-28, comprising
5 administering, to the animal, a non-pathogenic microorganism or virus which is carrying a nucleic acid fragment encoding and expressing the at least one modified CEA polypeptide.

36. The method according to claim 35, wherein the non-pathogenic microorganism or virus is administered once to the ani-
10 mal.

37. The method according to any one of claims 1-28, comprising administering, to the animal, at least one nucleic acid fragment which encodes and expresses the at least one modified CEA polypeptide.

15 38. The method according to claim 37, wherein the at least one nucleic acid fragment is selected from naked DNA, DNA formulated with charged or uncharged lipids, DNA formulated in liposomes, emulsified DNA, DNA included in a viral vector, DNA formulated with a transfection-facilitating protein or poly-
20 peptide, DNA formulated with a targeting protein or polypeptide, DNA formulated with a targeting carbohydrate, DNA formulated with Calcium precipitating agents, DNA coupled to an inert carrier molecule, and DNA formulated with an adjuvant.

39. The method according to claim 38, wherein the adjuvant is
25 selected from the group consisting of the adjuvants defined in any one of claims 31 or 32.

40. The method according to any claim 38 or 39, wherein the mode of administration is as defined in claim 33 or 34.

41. A modified human CEA polypeptide that is capable of inducing an immune response against autologous CEA in a human subject, comprising at least about 80 CEA-derived amino acids, either in the form of at least about 80 consecutive CEA-de-

5   rived amino acids or in the form of at least about 80 amino acids constituted of uninterrupted CEA-derived CTL epitopes, and at least one first non-human T helper epitope (T_H epitope).

42. The modified human CEA polypeptide according to claim 41, wherein the at least one foreign T_H epitope is present as an

10   insertion in the CEA amino acid sequence or as a substitution of part of the CEA amino acid sequence or as the result of deletion of part of the CEA amino acid sequence.

43. The modified human CEA according to claim 41 or 42, comprising at least 100 CEA derived amino acids, such as at least

15   , such as at least about 120, 140, 160 or 180 amino acids, preferably at least about 200, such as at least about 220, 250, 300, 400, or 500 amino acids.

44. The modified human CEA according to any one of claims 41-43, which comprises at least one substantially preserved CEA

20   domain.

45. The modified human CEA according to claim 44, which comprises at least 3 substantially preserved CEA domains, preferably domains 1-3.

46. The modified human CEA according to claim 45, comprising

25   all 7 CEA domains in substantially preserved form.

47. The modified human CEA according to any one of claims 41-46, wherein the at least one foreign T_H epitope is introduced in any one of the following regions of CEA:

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- between the C-terminal membrane anchor and domain 7

- in the loop structures in any one of domains 1-7 as shown in Fig. 1, and

between any two adjacent loops in CEA.

5 48. An immunogenic composition which comprises, as an effective immunogenic agent the modified human CEA according to any one of claims 41-47 in admixture with a pharmaceutically and immunologically acceptable carrier or vehicle, and optionally an adjuvant.

10 49. A nucleic acid fragment which encodes a modified CEA polypeptide according to any one of claims 41-47.

50. A vector carrying the nucleic acid fragment according to claim 49.

51. The vector according to claim 50 being capable of autono-
15 mous replication.

52. The vector according to claim 50 or 51 being selected from the group consisting of a plasmid, a phage, a cosmid, a mini-chromosome, and a virus.

53. The vector according to any one of claims 50-52, compri-
20 sing, in the 5'→3' direction and in operable linkage, a promoter for driving expression of the nucleic acid fragment according to claim 49, optionally a nucleic acid sequence encoding a leader peptide enabling secretion of or integration into the membrane of the polypeptide fragment, the nucleic
25 acid fragment according to claim 49, and optionally a nucleic acid sequence encoding a terminator.

54. The vector according to any one of claims 50-53 which, when introduced into a host cell, is integrated in the host cell genome or is not capable of being integrated in the host cell genome.

5 55. A transformed cell carrying the vector of any one of claims 50-54.

56. A composition for inducing production of antibodies a- gainst CEA, the composition comprising

- a nucleic acid fragment according to claim 49 or a vector
10   according to any one of claims 50-54, and

- a pharmaceutically and immunologically acceptable diluent and/or vehicle and/or adjuvant.

57. A stable cell line which carries the vector according to any one of claims 50-54 and which expresses the nucleic acid
15 fragment according to claim 49, and which optionally secretes or carries the modified CEA according to any one of claims 41- 47 on its surface.

58. A method for the preparation of the cell line according to claim 57, the method comprising transforming a host cell with
20 the nucleic acid fragment according to claim 49 or with the vector according to any one of claims 50-54.

1/2

Domain	Region	Struct. Design	MHC class I corr.
1	N-term	K35	K35
	Loop 1	R72-G75	R72-G75
	Linker 1	P142	P145
2	Loop 2	N182-L185	N182-S184 *
	Linker 2	P237	P237
3	Loop 3	N274-F277	Ø
	Linker 3	P322	Ø
4	Loop 4	N360-L363	N360-S362*
	Linker 4	P415	P415
5	Loop 5	D452-I455	D452-N454
	Linker 5	A498	A498
6	Loop 6	G538-L541	G538-S540
	Linker 6	P593	P593
7	Loop 7	N630-P633	N630-G631
	C-term.	S677	S677

Fig. 1

2/2

Fig 2

1
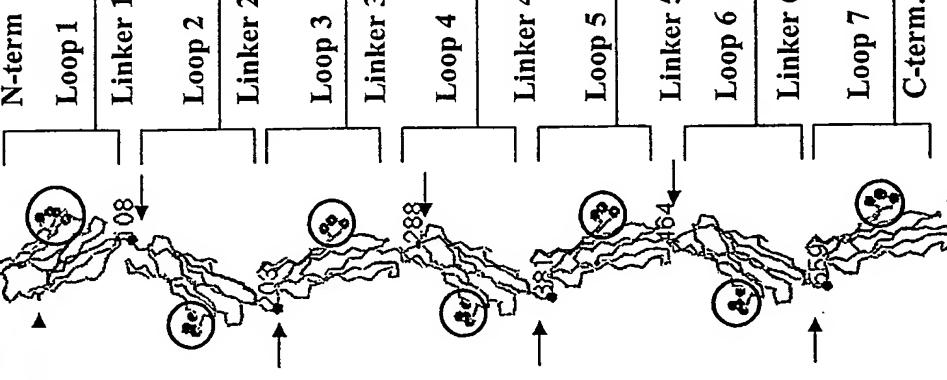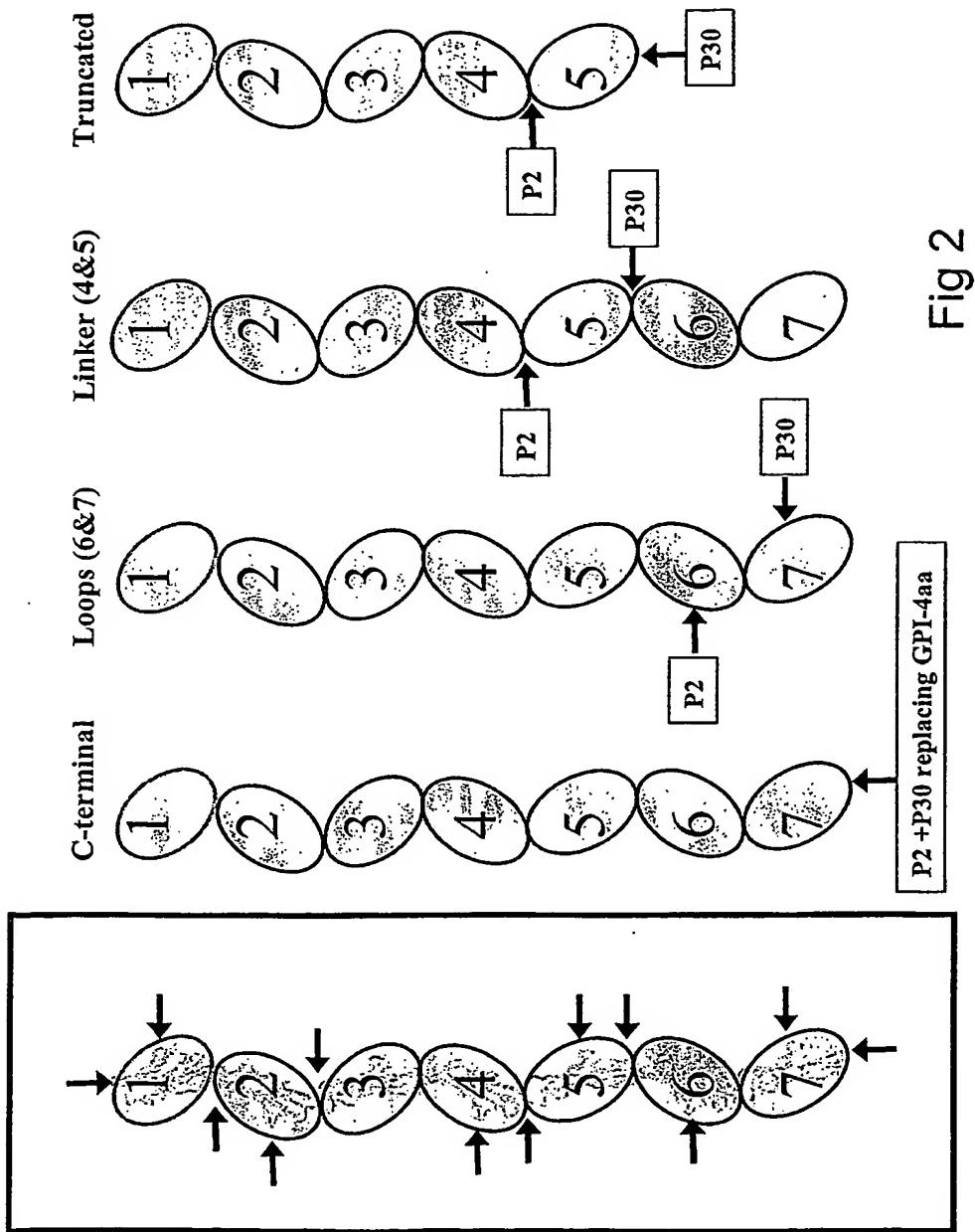
SEQUENCE LISTING

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<170> PatentIn version 3.2

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tcctggaact caagctcttc tccacagagg aggacagagc agacagcaga gacc atg   117
                                                           Met

gag tct ccc tcg gcc cct ccc cac aga tgg tgc atc ccc tgg cag agg   165
Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln Arg
        -30   -25   -20

ctc ctg ctc aca gcc tca ctt cta acc ttc tgg aac ccg ccc acc act   213
Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr Thr
        -15   -10   -5

gcc aag ctc act att gaa tcc acg ccg ttc aat gtc gca gag ggg aag   261
Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys
-1 1   5   10   15

gag gtg ctt cta ctt gtc cac aat ctg ccc cag cat ctt ttt ggc tac   309
Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly Tyr
                20   25   30

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agc tgg tac aaa ggt gaa aga gtg gat ggc aac cgt caa att ata gga    357
Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile Gly
            35              40                  45

tat gta ata gga act caa caa gct acc cca ggg ccc gca tac agt ggt    405
Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser Gly
        50                  55                  60

cga gag ata ata tac ccc aat gca tcc ctg ctg atc cag aac atc atc    453
Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile Ile
        65                  70              75

cag aat gac aca gga ttc tac acc cta cac gtc ata aag tca gat ctt    501
Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp Leu
80                  85              90                  95

gtg aat gaa gaa gca act ggc cag ttc cgg gta tac ccg gag ctg ccc    549
Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu Pro
                100                 105                 110

aag ccc tcc atc tcc agc aac aac tcc aaa ccc gtg gag gac aag gat    597
Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys Asp
            115                 120                 125

gct gtg gcc ttc acc tgt gaa cct gag act cag gac gca acc tac ctg    645
Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr Leu
            130                 135                 140

tgg tgg gta aac aat cag agc ctc ccg gtc agt ccc agg ctg cag ctg    693
Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu
            145                 150                 155

tcc aat ggc aac agg acc ctc act cta ttc aat gtc aca aga aat gac    741
Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn Asp
160                 165                 170                 175

aca gca agc tac aaa tgt gaa acc cag aac cca gtg agt gcc agg cgc    789
Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg Arg
            180                 185                 190

agt gat tca gtc atc ctg aat gtc ctc tat ggc ccg gat gcc ccc acc    837
Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro Thr
            195                 200                 205

att tcc cct cta aac aca tct tac aga tca ggg gaa aat ctg aac ctc    885
Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn Leu
            210                 215                 220

tcc tgc cac gca gcc tct aac cca cct gca cag tac tct tgg ttt gtc    933
Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe Val
            225                 230                 235

aat ggg act ttc cag caa tcc acc caa gag ctc ttt atc ccc aac atc    981
Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile
240                 245                 250                 255

act gtg aat aat agt gga tcc tat acg tgc caa gcc cat aac tca gac   1029
Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser Asp
                260                 265                 270
```

```
act ggc ctc aat agg acc aca gtc acg acg atc aca gtc tat gca gag    1077
Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala Glu
            275             280             285

cca ccc aaa ccc ttc atc acc agc aac aac tcc aac ccc gtg gag gat    1125
Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu Asp
            290             295             300

gag gat gct gta gcc tta acc tgt gaa cct gag att cag aac aca acc    1173
Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr Thr
            305             310             315

tac ctg tgg tgg gta aat aat cag agc ctc ccg gtc agt ccc agg ctg    1221
Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu
320             325             330             335

cag ctg tcc aat gac aac agg acc ctc act cta ctc agt gtc aca agg    1269
Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg
            340             345             350

aat gat gta gga ccc tat gag tgt gga atc cag aac gaa tta agt gtt    1317
Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser Val
            355             360             365

gac cac agc gac cca gtc atc ctg aat gtc ctc tat ggc cca gac gac    1365
Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Asp
            370             375             380

ccc acc att tcc ccc tca tac acc tat tac cgt cca ggg gtg aac ctc    1413
Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn Leu
385             390             395

agc ctc tcc tgc cat gca gcc tct aac cca cct gca cag tat tct tgg    1461
Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp
400             405             410             415

ctg att gat ggg aac atc cag caa cac aca caa gag ctc ttt atc tcc    1509
Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile Ser
            420             425             430

aac atc act gag aag aac agc gga ctc tat acc tgc cag gcc aat aac    1557
Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn Asn
            435             440             445

tca gcc agt ggc cac agc agg act aca gtc aag aca atc aca gtc tct    1605
Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val Ser
            450             455             460

gcg gag ctg ccc aag ccc tcc atc tcc agc aac aac tcc aaa ccc gtg    1653
Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val
            465             470             475

gag gac aag gat gct gtg gcc ttc acc tgt gaa cct gag gct cag aac    1701
Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln Asn
480             485             490             495
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4

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aca acc tac ctg tgg tgg gta aat ggt cag agc ctc cca gtc agt ccc      1749
Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro
            500                 505                 510

agg ctg cag ctg tcc aat ggc aac agg acc ctc act cta ttc aat gtc      1797
Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val
            515                 520                 525

aca aga aat gac gca aga gcc tat gta tgt gga atc cag aac tca gtg      1845
Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser Val
            530                 535                 540

agt gca aac cgc agt gac cca gtc acc ctg gat gtc ctc tat ggg ccg      1893
Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly Pro
            545                 550                 555

gac acc ccc atc att tcc ccc cca gac tcg tct tac ctt tcg gga gcg      1941
Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly Ala
560                 565                 570                 575

aac ctc aac ctc tcc tgc cac tcg gcc tct aac cca tcc ccg cag tat      1989
Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln Tyr
                580                 585                 590

tct tgg cgt atc aat ggg ata ccg cag caa cac aca caa gtt ctc ttt      2037
Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu Phe
                595                 600                 605

atc gcc aaa atc acg cca aat aat aac ggg acc tat gcc tgt ttt gtc      2085
Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe Val
            610                 615                 620

tct aac ttg gct act ggc cgc aat aat tcc ata gtc aag agc atc aca      2133
Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile Thr
            625                 630                 635

gtc tct gca tct gga act tct cct ggt ctc tca gct ggg gcc act gtc      2181
Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr Val
640                 645                 650                 655

ggc atc atg att gga gtg ctg gtt ggg gtt gct ctg ata tagcagccct      2230
Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
                660                 665

ggtgtagttt cttcatttca ggaagactga cagttgtttt gcttcttcct taaagcattt      2290

gcaacagcta cagtctaaaa ttgcttcttt accaaggata tttacagaaa agactctgac      2350

cagagatcga gaccatccta gccaacatcg tgaaacccca tctctactaa aaatacaaaa      2410

atgagctggg cttggtggcg cgcacctgta gtcccagtta ctcgggaggc tgaggcagga      2470

gaatcgcttg aacccgggag gtggagattg cagtgagccc agatcgcacc actgcactcc      2530

agtctggcaa cagagcaaga ctccatctca aaaagaaaag aaaagaagac tctgacctgt      2590

actcttgaat acaagtttct gataccactg cactgtctga gaatttccaa aactttaatg      2650

aactaactga cagcttcatg aaactgtcca ccaagatcaa gcagagaaaa taattaattt      2710
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catgggacta aatgaactaa tgaggattgc tgattcttta aatgtcttgt ttcccagatt   2770

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ttgtgaacaa aaattgagac atttacattt tctccctatg tggtcgctcc agacttggga   2890

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Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
              -15                 -10                  -5


Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
     -1  1            5                 10


Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
15                  20                 25                      30


Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
              35                 40                      45


Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
              50                 55                 60


Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
     65                 70                 75


Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
     80                 85                 90


Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
95                  100                105                   110


Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
              115                120                125
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6

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Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
        130               135               140

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
        145               150               155

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
    160               165               170

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
175               180               185               190

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
            195               200               205

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
            210               215               220

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
        225               230               235

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
        240               245               250

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
255               260               265               270

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
            275               280               285

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
            290               295               300

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
        305               310               315

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
    320               325               330

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
335               340               345               350

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
            355               360               365
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Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
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Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
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Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
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Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
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Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
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Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
            450   455   460

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
        465   470   475

Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
    480   485   490

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
495   500   505   510

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
                515   520   525

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
            530   535   540

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
        545   550   555

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
        560   565   570

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
575   580   585   590

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
            595   600   605

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Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
            610             615         620

Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
        625             630             635

Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
    640             645             650 .

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile         .
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       expression


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cct tgg cag cgc ctg ctc ctg aca gca agc ctg ctg acc ttt tgg aat        97
Pro Trp Gln Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn
    -20             -15             -10

cca ccc acg aca gcc aaa ctg act atc gag tct act cct ttc aac gtg       145
Pro Pro Thr Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val
-5              -1  1           5                   10

gcg gaa ggg aag gag gtt ctg ctc ctg gtc cat aat ctg cca cag cac       193
Ala Glu Gly Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His
            15              20              25
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ctg ttt ggt tat tca tgg tac aaa ggc gaa cgc gtg gat gga aac cgg          241
Leu Phe Gly Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg
        30              35                  40

caa att atc ggg tat gtt atc ggc aca cag cag gcc aca ccc ggt ccg          289
Gln Ile Ile Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro
        45              50                  55

gct tac agt ggg cgc gaa att atc tat cca aat gcc agc ctg ctg atc          337
Ala Tyr Ser Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile
60              65                  70                  75

caa aac att atc cag aat gac act ggc ttc tac aca ctg cat gtc atc          385
Gln Asn Ile Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile
                80                  85                  90

aaa agc gat ctg gtg aac gag gaa gca acg ggt cag ttt cgg gtt tat          433
Lys Ser Asp Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr
                95                  100                 105

ccc gaa ctg cct aag cca tca att tct tcc aat aac agt aaa ccc gtc          481
Pro Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val
        110                 115                 120

gaa gac aaa gac gcc gtg gct ttc acg tgc gag cct gaa aca caa gat          529
Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp
        125                 130                 135

gca act tac ctg tgg tgg gtt aac aat cag agc ctg cca gtc tca ccc          577
Ala Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro
140                 145                 150                 155

cgc ctg cag ctg agc aac gga aat cgg acc ctg aca ctc ttt aac gtg          625
Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val
                160                 165                 170

acg cgc aat gac act gcc tct tat aag tgt gag aca caa aac cct gtt          673
Thr Arg Asn Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val
                175                 180                 185

tca gcg cgg cgc agc gat agt gtt atc ctg aat gtg ctg tac ggc cca          721
Ser Ala Arg Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro
        190                 195                 200

gac gct ccc acc att tcc ccg ctg aac act tct tat cgc tca ggg gaa          769
Asp Ala Pro Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu
        205                 210                 215

aat ctg aac ctg agc tgc cac gcc gca agc aat cca ccc gcg cag tac          817
Asn Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr
220                 225                 230                 235

agt tgg ttc gtc aac ggt aca ttt cag caa tct act cag gaa ctg ttc          865
Ser Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe
                240                 245                 250

atc cct aat att acg gtt aac aat tca ggc agc tat aca tgt cag gct          913
Ile Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala
                255                 260                 265
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10

```
cat aac tcc gac aca ggg ctg aat cgg act aca gtg acg acg atc aca        961
His Asn Ser Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr
            270             275             280

gtc tac gcc gag cca ccc aaa ccc ttt att act tct aac aat agt aac       1009
Val Tyr Ala Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn
            285             290             295

cca gtt gaa gat gag gac gca gtg gct ctg acc tgc gaa cct gag atc       1057
Pro Val Glu Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile
300             305             310             315

caa aat aca acc tat ctg tgg tgg gtc aac aat cag tca ctg cca gtt       1105
Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val
            320             325             330

agc ccc cgc ctg cag ctc agc aac gac aat cgg act ctg acg ctg ctc       1153
Ser Pro Arg Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu
            335             340             345

tct gtg aca cgc aac gat gtc ggt cca tac gaa tgt ggc att caa aat       1201
Ser Val Thr Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn
            350             355             360

gaa ctg tca gtt gac cac agt gat ccc gtg atc ctg aac gtc ctg tat       1249
Glu Leu Ser Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr
            365             370             375

gga cca gac gac cct acc att agc cca tcc tac act tat tac cgg ccc       1297
Gly Pro Asp Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro
380             385             390             395

ggg gtt aat ctg tct ctg agc tgc cat gcc gcg tca aac cca ccc gca       1345
Gly Val Asn Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala
            400             405             410

cag tac agc tgg ctg atc gat ggc aat att cag caa cac aca cag gag       1393
Gln Tyr Ser Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu
            415             420             425

ctg ttc atc agt aac att aca gaa aaa aat tct gga ctg tat acg tgt       1441
Leu Phe Ile Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys
            430             435             440

cag gct aac aat tcc gcc agc ggt cat agc cgc aca act gtg aag acg       1489
Gln Ala Asn Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr
            445             450             455

atc act gtc tct gcc gag ctg ccg aaa cca agt att tca tcc aac aat       1537
Ile Thr Val Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn
460             465             470             475

agc aag ccc gtt gaa gac aaa gat gca gtg gcc ttt aca tgc gag cca       1585
Ser Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro
            480             485             490
```

```
gaa gct caa aac act acg tac ctg tgg tgg gtc aat ggc cag tct ctg     1633
Glu Ala Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu
            495                 500             505

ccc gtt agc cca cgg ctc cag ctg agt aac ggg aat cgc aca ctg acc     1681
Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr
            510                 515             520

ctg ttc aac gtg acc cgg aat gac gcg cgc gcc tat gtc tgt gga atc     1729
Leu Phe Asn Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile
            525                 530             535

caa aac tcc gtt agc gca aat cgg tct gac cct gtg aca ctg gat gtc     1777
Gln Asn Ser Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val
540             545                 550             555

ctg tac ggc cca gac act ccc att atc tca cca ccc gat agc agt tat     1825
Leu Tyr Gly Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr
            560                 565             570

ctg agc ggt gct aac ctg aat ctc tct tgc cac tcc gcc tca aac cct     1873
Leu Ser Gly Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro
            575                 580             585

tct cca cag tac agc tgg cgc atc aat ggg att ccc cag caa cat acg     1921
Ser Pro Gln Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr
            590                 595             600

cag gtt ctg ttt atc gca aaa att aca cca aac aat aac ggc acc tat     1969
Gln Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr
            605                 610             615

gcg tgt ttc gtg agt aac ctg gcc act gga cgg aat aac agc atc gtc     2017
Ala Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val
620             625                 630             635

aag tcc att aca gtt tct gca agc ggt acg tca ccc taatga              2059
Lys Ser Ile Thr Val Ser Ala Ser Gly Thr Ser Pro
            640                 645
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<210> 4
<211> 681
<212> PRT
<213> Artificial sequence

<220>
<223> Human CEA-encoding DNA sequence codon optimized for non-human
      expression

<400> 4

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
            -30             -25             -20


Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
        -15             -10             -5
```

```
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
    -1  1           5               10

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
15          20              25                  30

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
            35              40                  45

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
        50              55              60

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
    65              70                  75

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
    80              85              90

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
95              100             105                 110

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
            115             120                 125

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
        130             135             140

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
    145             150             155

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
    160             165             170

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
175             180             185                 190

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
            195             200             205

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
            210             215             220

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
    225             230             235
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13

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
240   245   250

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
255   260   265   270

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
                275   280   285

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                290   295   300

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
        305   310   315

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
    320   325   330

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
335   340   345   350

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
                355   360   365

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
            370   375   380

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
        385   390   395

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
    400   405   410

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
415   420   425   430

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
                435   440   445

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
            450   455   460

14

```
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
        465             470             475


Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
    480             485             490


Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
495             500             505             510


Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
            515             520             525


Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
        530             535             540


Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
    545             550             555


Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
560             565             570


Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
575             580             585             590


Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
            595             600             605


Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
            610             615             620


Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
    625             630             635


Thr Val Ser Ala Ser Gly Thr Ser Pro
    640             645
```

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<210>  5
<211>  2167
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Human CEA with introduction of tetanus toxoid P2 and P30 epitopes


<220>
<221>  CDS
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15

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<222>    (11)..(2161)

<220>
<221>   sig_peptide
<222>   (11)..(112)

<220>
<221>   mat_peptide
<222>   (113)..(2161)

<220>
<221>   misc_feature
<222>   (2042)..(2086)
<223>   Tetanus toxoid P2 epitope

<220>
<221>   misc_feature
<222>   (2087)..(2149)
<223>   Tetanus toxoid P30 epitope

<400>   5
gctagccacc atg gaa agt ccc tca gcc cca ccc cac cgc tgg tgt att          49
           Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile
                    -30                     -25

cct tgg cag cgc ctg ctc ctg aca gca agc ctg ctg acc ttt tgg aat       97
Pro Trp Gln Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn
    -20              -15              -10

cca ccc acg aca gcc aaa ctg act atc gag tct act cct ttc aac gtg     145
Pro Pro Thr Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val
-5               -1  1            5                       10

gcg gaa ggg aag gag gtt ctg ctc ctg gtc cat aat ctg cca cag cac     193
Ala Glu Gly Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His
              15               20               25

ctg ttt ggt tat tca tgg tac aaa ggc gaa cgc gtg gat gga aac cgg     241
Leu Phe Gly Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg
           30               35               40

caa att atc ggg tat gtt atc ggc aca cag cag gcc aca ccc ggt ccg     289
Gln Ile Ile Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro
    45                   50               55

gct tac agt ggg cgc gaa att atc tat cca aat gcc agc ctg ctg atc     337
Ala Tyr Ser Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile
60                   65               70                   75

caa aac att atc cag aat gac act ggc ttc tac aca ctg cat gtc atc     385
Gln Asn Ile Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile
                80               85               90

aaa agc gat ctg gtg aac gag gaa gca acg ggt cag ttt cgg gtt tat     433
Lys Ser Asp Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr
                95               100              105
```

```
ccc gaa ctg cct aag cca tca att tct tcc aat aac agt aaa ccc gtc      481
Pro Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val
        110             115                 120

gaa gac aaa gac gcc gtg gct ttc acg tgc gag cct gaa aca caa gat      529
Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp
    125             130.                135

gca act tac ctg tgg tgg gtt aac aat cag agc ctg cca gtc tca ccc      577
Ala Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro
140             145                 150                 155

cgc ctg cag ctg agc aac gga aat cgg acc ctg aca ctc ttt aac gtg      625
Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val
            160                 165                 170

acg cgc aat gac act gcc tct tat aag tgt gag aca caa aac cct gtt      673
Thr Arg Asn Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val
            175                 180                 185

tca gcg cgg cgc agc gat agt gtt atc ctg aat gtg ctg tac ggc cca      721
Ser Ala Arg Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro
        190                 195                 200

gac gct ccc acc att tcc ccg ctg aac act tct tat cgc tca ggg gaa      769
Asp Ala Pro Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu
        205                 210                 215

aat ctg aac ctg agc tgc cac gcc gca agc aat cca ccc gcg cag tac      817
Asn Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr
220                 225                 230                 235

agt tgg ttc gtc aac ggt aca ttt cag caa tct act cag gaa ctg ttc      865
Ser Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe
                240                 245                 250

atc cct aat att acg gtt aac aat tca ggc agc tat aca tgt cag gct      913
Ile Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala
                255             .   260                 265

cat aac tcc gac aca ggg ctg aat cgg act aca gtg acg acg atc aca      961
His Asn Ser Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr
            270                 275                 280

gtc tac gcc gag cca ccc aaa ccc ttt att act tct aac aat agt aac     1009
Val Tyr Ala Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn
        285                 290                 295

cca gtt gaa gat gag gac gca gtg gct ctg acc tgc gaa cct gag atc     1057
Pro Val Glu Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile
300                 305                 310                 315

caa aat aca acc tat ctg tgg tgg gtc aac aat cag tca ctg cca gtt     1105
Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val
                320                 325                 330

agc ccc cgc ctg cag ctc agc aac gac aat cgg act ctg acg ctg ctc     1153
Ser Pro Arg Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu
            335                 340                 345
```

17

```
tct gtg aca cgc aac gat gtc ggt cca tac gaa tgt ggc att caa aat      1201
Ser Val Thr Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn
        350             355             360

gaa ctg tca gtt gac cac agt gat ccc gtg atc ctg aac gtc ctg tat      1249
Glu Leu Ser Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr
    365             370             375

gga cca gac gac cct acc att agc cca tcc tac act tat tac cgg ccc      1297
Gly Pro Asp Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro
380             385             390             395

ggg gtt aat ctg tct ctg agc tgc cat gcc gcg tca aac cca ccc gca      1345
Gly Val Asn Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala
                400             405             410

cag tac agc tgg ctg atc gat ggc aat att cag caa cac aca cag gag      1393
Gln Tyr Ser Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu
            415             420             425

ctg ttc atc agt aac att aca gaa aaa aat tct gga ctg tat acg tgt      1441
Leu Phe Ile Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys
        430             435             440

cag gct aac aat tcc gcc agc ggt cat agc cgc aca act gtg aag acg      1489
Gln Ala Asn Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr
    445             450             455

atc act gtc tct gcc gag ctg ccg aaa cca agt att tca tcc aac aat      1537
Ile Thr Val Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn
460             465             470             475

agc aag ccc gtt gaa gac aaa gat gca gtg gcc ttt aca tgc gag cca      1585
Ser Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro
                480             485             490

gaa gct caa aac act acg tac ctg tgg tgg gtc aat ggc cag tct ctg      1633
Glu Ala Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu
            495             500             505

ccc gtt agc cca cgg ctc cag ctg agt aac ggg aat cgc aca ctg acc      1681
Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr
        510             515             520

ctg ttc aac gtg acc cgg aat gac gcg cgc gcc tat gtc tgt gga atc      1729
Leu Phe Asn Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile
    525             530             535

caa aac tcc gtt agc gca aat cgg tct gac cct gtg aca ctg gat gtc      1777
Gln Asn Ser Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val
540             545             550             555

ctg tac ggc cca gac act ccc att atc tca cca ccc gat agc agt tat      1825
Leu Tyr Gly Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr
                560             565             570

ctg agc ggt gct aac ctg aat ctc tct tgc cac tcc gcc tca aac cct      1873
Leu Ser Gly Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro
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18

	575				580					585				

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          575                    580                      585
tct cca cag tac agc tgg cgc atc aat ggg att ccc cag caa cat acg      1921
Ser Pro Gln Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr
        590                 595                 600

cag gtt ctg ttt atc gca aaa att aca cca aac aat aac ggc acc tat      1969
Gln Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr
        605                 610                 615

gcg tgt ttc gtg agt aac ctg gcc act gga cgg aat aac agc atc gtc      2017
Ala Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val
620                 625                 630                 635

aag tcc att aca gtt tct gca agc cag tac atc aaa gct aac tcc aaa      2065
Lys Ser Ile Thr Val Ser Ala Ser Gln Tyr Ile Lys Ala Asn Ser Lys
                640                 645                 650

ttc atc ggc atc acc gaa ctg ttc aac aac ttc acc gtt tcc ttc tgg      2113
Phe Ile Gly Ile Thr Glu Leu Phe Asn Asn Phe Thr Val Ser Phe Trp
                655                 660                 665

ctg cgc gtt cca aaa gtt tcc gct tcc cac ctg gaa ggt acg tca ccc      2161
Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gly Thr Ser Pro
                670                 675                 680

                                                                     2167
taatga
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<210> 6
<211> 717
<212> PRT
<213> Artificial sequence

<220>
<223> Human CEA with introduction of tetanus toxoid P2 and P30 epitopes

<400> 6

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
              -30             -25                 -20

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
          -15             -10                 -5

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
    -1  1               5                   10

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
15                  20                  25                  30

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
                35                  40                  45
```

19

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
            50   55   60

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
        65   70   75

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
    80   85   90

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
95   100   105   110

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
                115   120   125

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
            130   135   140

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
    145   150   155

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
    160   165   170

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
175   180   185   190

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
            195   200   205

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
            210   215   220

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
        225   230   235

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
    240   245   250

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
255   260   265   270

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
            275   280   285

20

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
        290   295   300

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
        305   310   315

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
    320   325   330   .

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
335   340   345   350

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
            355   360   365

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
            370   375   380

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
        385   .   390   395

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
    400   405   410

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
415   420   425   430

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
            435   440   .   445

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
            450   455   460

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
    465   470   475

Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
    480   485   490

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
495   500   505   510

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
            515   520   525

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Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
        530             535             540

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
        545             550             555

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
    560             565             570

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
575             580             585             590

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
            595             600             605

Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
            610             615             620

Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
        625             630             635

Thr Val Ser Ala Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
    640             645             650

Ile Thr Glu Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
655             660             665             670

Pro Lys Val Ser Ala Ser His Leu Glu Gly Thr Ser Pro
            675             680
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<210> 7
<211> 2140
<212> DNA
<213> Artificial sequence

<220>
<223> Human CEA with introduction of tetanus toxoid P2 and P30 epitopes

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<221> CDS
<222> (11)..(2134)

<220>
<221> sig_peptide
<222> (11)..(112)

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<221>  mat_peptide
<222>  (113)..(2134)

<220>
<221>  misc_feature
<222>  (1622)..(1666)
<223>  Tetanus toxoid P2 epitope

<220>
<221>  misc_feature
<222>  (1934)..(1696)
<223>  Tetanus toxoid P30 epitope

<400>  7
gctagccacc atg gaa agt ccc tca gcc cca ccc cac cgc tgg tgt att          49
           Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile
                       -30                  -25

cct tgg cag cgc ctg ctc ctg aca gca agc ctg ctg acc ttt tgg aat          97
Pro Trp Gln Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn
    -20               -15                  -10

cca ccc acg aca gcc aaa ctg act atc gag tct act cct ttc aac gtg          145
Pro Pro Thr Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val
-5              -1  1              5                  10

gcg gaa ggg aag gag gtt ctg ctc ctg gtc cat aat ctg cca cag cac          193
Ala Glu Gly Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His
            15                  20                  25

ctg ttt ggt tat tca tgg tac aaa ggc gaa cgc gtg gat gga aac cgg          241
Leu Phe Gly Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg
        30              35                  40

caa att atc ggg tat gtt atc ggc aca cag cag gcc aca ccc ggt ccg          289
Gln Ile Ile Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro
    45              50                  55

gct tac agt ggg cgc gaa att atc tat cca aat gcc agc ctg ctg atc          337
Ala Tyr Ser Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile
60              65                  70                  75

caa aac att atc cag aat gac act ggc ttc tac aca ctg cat gtc atc          385
Gln Asn Ile Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile
                80                  85                  90

aaa agc gat ctg gtg aac gag gaa gca acg ggt cag ttt cgg gtt tat          433
Lys Ser Asp Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr
            95                  100                 105

ccc gaa ctg cct aag cca tca att tct tcc aat aac agt aaa ccc gtc          481
Pro Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val
        110                 115                 120

gaa gac aaa gac gcc gtg gct ttc acg tgc gag cct gaa aca caa gat          529
Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp
        125                 130                 135
```

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gca act tac ctg tgg tgg gtt aac aat cag agc ctg cca gtc tca ccc      577
Ala Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro
140                 145                 150                 155

cgc ctg cag ctg agc aac gga aat cgg acc ctg aca ctc ttt aac gtg      625
Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val
                160                 165                 170

acg cgc aat gac act gcc tct tat aag tgt gag aca caa aac cct gtt      673
Thr Arg Asn Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val
            175                 180                 185

tca gcg cgg cgc agc gat agt gtt atc ctg aat gtg ctg tac ggc cca      721
Ser Ala Arg Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro
            190                 195                 200

gac gct ccc acc att tcc ccg ctg aac act tct tat cgc tca ggg gaa      769
Asp Ala Pro Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu
            205                 210                 215

aat ctg aac ctg agc tgc cac gcc gca agc aat cca ccc gcg cag tac      817
Asn Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr
220                 225                 230                 235

agt tgg ttc gtc aac ggt aca ttt cag caa tct act cag gaa ctg ttc      865
Ser Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe
                240                 245                 250

atc cct aat att acg gtt aac aat tca ggc agc tat aca tgt cag gct      913
Ile Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala
                255                 260                 265

cat aac tcc gac aca ggg ctg aat cgg act aca gtg acg acg atc aca      961
His Asn Ser Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr
            270                 275                 280

gtc tac gcc gag cca ccc aaa ccc ttt att act tct aac aat agt aac     1009
Val Tyr Ala Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn
285                 290                 295

cca gtt gaa gat gag gac gca gtg gct ctg acc tgc gaa cct gag atc     1057
Pro Val Glu Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile
300                 305                 310                 315

caa aat aca acc tat ctg tgg tgg gtc aac aat cag tca ctg cca gtt     1105
Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val
                320                 325                 330

agc ccc cgc ctg cag ctc agc aac gac aat cgg act ctg acg ctg ctc     1153
Ser Pro Arg Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu
            335                 340                 345

tct gtg aca cgc aac gat gtc ggt cca tac gaa tgt ggc att caa aat     1201
Ser Val Thr Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn
            350                 355                 360

gaa ctg tca gtt gac cac agt gat ccc gtg atc ctg aac gtc ctg tat     1249
Glu Leu Ser Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr
365                 370                 375
```

24

```
gga cca gac gac cct acc att agc cca tcc tac act tat tac cgg ccc       1297
Gly Pro Asp Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro
380                 385             390                 395

ggg gtt aat ctg tct ctg agc tgc cat gcc gcg tca aac cca ccc gca       1345
Gly Val Asn Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala
                400             405                 410

cag tac agc tgg ctg atc gat ggc aat att cag caa cac aca cag gag       1393
Gln Tyr Ser Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu
                415             420             425

ctg ttc atc agt aac att aca gaa aaa aat tct gga ctg tat acg tgt       1441
Leu Phe Ile Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys
            430             435             440

cag gct aac aat tcc gcc agc ggt cat agc cgc aca act gtg aag acg       1489
Gln Ala Asn Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr
        445             450             455

atc act gtc tct gcc gag ctg ccg aaa cca agt att tca tcc aac aat       1537
Ile Thr Val Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn
460             465             470             475

agc aag ccc gtt gaa gac aaa gat gca gtg gcc ttt aca tgc gag cca       1585
Ser Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro
                480             485             490

gaa gct caa aac act acg tac ctg tgg tgg gtc aat cag tac atc aaa       1633
Glu Ala Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Gln Tyr Ile Lys
                495             500             505

gct aac tcc aaa ttc atc ggc atc acc gaa ctg ctg ccc gtt agc cca       1681
Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Leu Pro Val Ser Pro
        510             515             520

cgg ctc cag ctg agt aac ggg aat cgc aca ctg acc ctg ttc aac gtg       1729
Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val
        525             530             535

acc cgg aat gac gcg cgc gcc tat gtc tgt gga atc caa aac tcc gtt       1777
Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser Val
540             545             550             555

agc gca aat cgg tct gac cct gtg aca ctg gat gtc ctg tac ggc cca       1825
Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly Pro
                560             565             570

gac act ccc att atc tca cca ccc gat agc agt tat ctg agc ggt gct       1873
Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly Ala
            575             580             585

aac ctg aat ctc tct tgc cac tcc gcc tca aac cct tct cca cag tac       1921
Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln Tyr
            590             595             600
```

```
agc tgg cgc atc ttc aac aac ttc acc gtt tcc ttc tgg ctg cgc gtt    1969
Ser Trp Arg Ile Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
    605             610             615

cca aaa gtt tcc gct tcc cac ctg gaa att ccc cag caa cat acg cag    2017
Pro Lys Val Ser Ala Ser His Leu Glu Ile Pro Gln Gln His Thr Gln
620             625             630             635

gtt ctg ttt atc gca aaa att aca cca aac aat aac ggc acc tat gcg    2065
Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala
            640             645             650

tgt ttc gtg agt aac ctg gcc act gga cgg aat aac agc atc gtc aag    2113
Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys
            655             660             665

tcc att aca gtt tct gca agc taatga                                 2140
Ser Ile Thr Val Ser Ala Ser
            670
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<210> 8
<211> 708
<212> PRT
<213> Artificial sequence

<220>
<223> Human CEA with introduction of tetanus toxoid P2 and P30 epitopes

<400> 8

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
            -30             -25             -20

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
        -15             -10             -5

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
    -1  1           5               10

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
15              20              25              30

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
            35              40              45

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
            50              55              60

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
            65              70              75
```

26

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
    80   85   90

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
95   100   105   110

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
            115   120   125

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
            130   135   140

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
        145   150   155

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
    160   165   170

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
175   180   185   190

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
            195   200   205

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
            210   215   220

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
        225   230   235

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
    240   245   250

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
255   260   265   270

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
            275   280   285

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
            290   295   300

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
    305   310   315

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
    320   325   330

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
335   340   345   350

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
                355   360   365

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
            370   375   380

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
        385   390   395

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
    400   405   410

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
415   420   425   430

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
            435   440   445

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
            450   455   460

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
    465   470   475

Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
    480   485   490

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gln Tyr Ile Lys Ala Asn Ser
495   500   505   510

Lys Phe Ile Gly Ile Thr Glu Leu Leu Pro Val Ser Pro Arg Leu Gln
            515   520   525

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
            530   535   540

Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser Val Ser Ala Asn
    545   550   555

```
Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly Pro Asp Thr Pro
    560             565             570

Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly Ala Asn Leu Asn
575             580             585             590

Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln Tyr Ser Trp Arg
            595             600             605

Ile Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val
            610             615             620

Ser Ala Ser His Leu Glu Ile Pro Gln Gln His Thr Gln Val Leu Phe
            625             630             635

Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe Val
    640             645             650

Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile Thr
655             660             665             670

Val Ser Ala Ser
```

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<210>   9
<211>   2155
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Human CEA with introduction of tetanus toxoid P2 and P30 epitopes

<220>
<221>   CDS
<222>   (11)..(2149)

<220>
<221>   sig_peptide
<222>   (11)..(112)

<220>
<221>   mat_peptide
<222>   (113)..(2149)

<220>
<221>   misc_feature
<222>   (1253)..(1297)
<223>   Tetanus toxoid P2 epitope
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<220>
<221> misc_feature
<222> (1547)..(1609)
<223> Tetanus toxoid P30 epitope

<400> 9
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gctagccacc atg gaa agt ccc tca gcc cca ccc cac cgc tgg tgt att      . 49
           Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile
               -30              -25

cct tgg cag cgc ctg ctc ctg aca gca agc ctg ctg acc ttt tgg aat      97
Pro Trp Gln Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn
    -20              -15                   -10

cca ccc acg aca gcc aaa ctg act atc gag tct act cct ttc aac gtg     145
Pro Pro Thr Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val
-5               -1  1               5                   10

gcg gaa ggg aag gag gtt ctg ctc ctg gtc cat aat ctg cca cag cac     193
Ala Glu Gly Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His
              15                   20                   25

ctg ttt ggt tat tca tgg tac aaa ggc gaa cgc gtg gat gga aac cgg     241
Leu Phe Gly Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg
        30                   35                   40

caa att atc ggg tat gtt atc ggc aca cag cag gcc aca ccc ggt ccg     289
Gln Ile Ile Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro
    45                   50                   55

gct tac agt ggg cgc gaa att atc tat cca aat gcc agc ctg ctg atc     337
Ala Tyr Ser Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile
60                   65                   70                   75

caa aac att atc cag aat gac act ggc ttc tac aca ctg cat gtc atc     385
Gln Asn Ile Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile
                  80                   85                   90

aaa agc gat ctg gtg aac gag gaa gca acg ggt cag ttt cgg gtt tat     433
Lys Ser Asp Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr
              95                   100                  105

ccc gaa ctg cct aag cca tca att tct tcc aat aac agt aaa ccc gtc     481
Pro Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val
        110                  115                  120

gaa gac aaa gac gcc gtg gct ttc acg tgc gag cct gaa aca caa gat     529
Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp
        125                  130                  135

gca act tac ctg tgg tgg gtt aac aat cag agc ctg cca gtc tca ccc     577
Ala Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro
140                  145                  150                  155

cgc ctg cag ctg agc aac gga aat cgg acc ctg aca ctc ttt aac gtg     625
Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val
              160                  165                  170
```

```
acg cgc aat gac act gcc tct tat aag tgt gag aca caa aac cct gtt        673
Thr Arg Asn Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val
            175             180                 185

tca gcg cgg cgc agc gat agt gtt atc ctg aat gtg ctg tac ggc cca        721
Ser Ala Arg Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro
        190             195                 200

gac gct ccc acc att tcc ccg ctg aac act tct tat cgc tca ggg gaa        769
Asp Ala Pro Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu
        205             210             215

aat ctg aac ctg agc tgc cac gcc gca agc aat cca ccc gcg cag tac        817
Asn Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr
220             225             230             235

agt tgg ttc gtc aac ggt aca ttt cag caa tct act cag gaa ctg ttc        865
Ser Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe
            240             245             250

atc cct aat att acg gtt aac aat tca ggc agc tat aca tgt cag gct        913
Ile Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala
            255             260             265

cat aac tcc gac aca ggg ctg aat cgg act aca gtg acg acg atc aca        961
His Asn Ser Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr
            270             275             280

gtc tac gcc gag cca ccc aaa ccc ttt att act tct aac aat agt aac       1009
Val Tyr Ala Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn
            285             290             295

cca gtt gaa gat gag gac gca gtg gct ctg acc tgc gaa cct gag atc       1057
Pro Val Glu Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile
300             305             310             315

caa aat aca acc tat ctg tgg tgg gtc aac aat cag tca ctg cca gtt       1105
Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val
            320             325             330

agc ccc cgc ctg cag ctc agc aac gac aat cgg act ctg acg ctg ctc       1153
Ser Pro Arg Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu
            335             340             345

tct gtg aca cgc aac gat gtc ggt cca tac gaa tgt ggc att caa aat       1201
Ser Val Thr Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn
            350             355             360

gaa ctg tca gtt gac cac agt gat ccc gtg atc ctg aac gtc ctg tat       1249
Glu Leu Ser Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr
            365             370             375

gga cag tac atc aaa gct aac tcc aaa ttc atc ggc atc acc gaa ctg       1297
Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
380             385             390             395

cca gac gac cct acc att agc cca tcc tac act tat tac cgg ccc ggg       1345
Pro Asp Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly
            400             405             410
```

31

```
gtt aat ctg tct ctg agc tgc cat gcc gcg tca aac cca ccc gca cag      1393
Val Asn Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln
            415                 420                 425

tac agc tgg ctg atc gat ggc aat att cag caa cac aca cag gag ctg      1441
Tyr Ser Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu
            430                 435                 440

ttc atc agt aac att aca gaa aaa aat tct gga ctg tat acg tgt cag      1489
Phe Ile Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln
            445                 450                 455

gct aac aat tcc gcc agc ggt cat agc cgc aca act gtg aag acg atc      1537
Ala Asn Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile
460                 465                 470                 475

act gtc tct ttc aac aac ttc acc gtt tcc ttc tgg ctg cgc gtt cca      1585
Thr Val Ser Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
                480                 485                 490

aaa gtt tcc gct tcc cac ctg gaa gcc gag ctg ccg aaa cca agt att      1633
Lys Val Ser Ala Ser His Leu Glu Ala Glu Leu Pro Lys Pro Ser Ile
                495                 500                 505

tca tcc aac aat agc aag ccc gtt gaa gac aaa gat gca gtg gcc ttt      1681
Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe
                510                 515                 520

aca tgc gag cca gaa gct caa aac act acg tac ctg tgg tgg gtc aat      1729
Thr Cys Glu Pro Glu Ala Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn
                525                 530                 535

ggc cag tct ctg ccc gtt agc cca cgg ctc cag ctg agt aac ggg aat      1777
Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Gly Asn
540                 545                 550                 555

cgc aca ctg acc ctg ttc aac gtg acc cgg aat gac gcg cgc gcc tat      1825
Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn Asp Ala Arg Ala Tyr
                560                 565                 570

gtc tgt gga atc caa aac tcc gtt agc gca aat cgg tct gac cct gtg      1873
Val Cys Gly Ile Gln Asn Ser Val Ser Ala Asn Arg Ser Asp Pro Val
                575                 580                 585

aca ctg gat gtc ctg tac ggc cca gac act ccc att atc tca cca ccc      1921
Thr Leu Asp Val Leu Tyr Gly Pro Asp Thr Pro Ile Ile Ser Pro Pro
                590                 595                 600

gat agc agt tat ctg agc ggt gct aac ctg aat ctc tct tgc cac tcc      1969
Asp Ser Ser Tyr Leu Ser Gly Ala Asn Leu Asn Leu Ser Cys His Ser
                605                 610                 615

gcc tca aac cct tct cca cag tac agc tgg cgc atc aat ggg att ccc      2017
Ala Ser Asn Pro Ser Pro Gln Tyr Ser Trp Arg Ile Asn Gly Ile Pro
620                 625                 630                 635
```

```
cag caa cat acg cag gtt ctg ttt atc gca aaa att aca cca aac aat    2065
Gln Gln His Thr Gln Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn
            640             645             650

aac ggc acc tat gcg tgt ttc gtg agt aac ctg gcc act gga cgg aat    2113
Asn Gly Thr Tyr Ala Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn
            655             660             665

aac agc atc gtc aag tcc att aca gtt tct gca agc taatga            2155
Asn Ser Ile Val Lys Ser Ile Thr Val Ser Ala Ser
            670             675
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<210> 10
<211> 713
<212> PRT
<213> Artificial sequence

<220>
<223> Human CEA with introduction of tetanus toxoid P2 and P30 epitopes

<400> 10

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
            -30             -25             -20

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            -15             -10             -5

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      -1  1               5               10

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
15              20              25              30

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
            35              40              45

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
            50              55              60

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
            65              70              75

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
            80              85              90

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
95              100             105             110
```

33

```
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
            115             120             125


Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
            130             135             140


Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            145             150             155


Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
    160             165             170


Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
175             180             185             190


Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
            195             200             205


Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
            210             215             220


Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
            225             230             235


Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
    240             245             250


Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
255             260             265             270


Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Ile Thr Val Tyr Ala
            275             280             285


Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
            290             295             300


Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
        305             310             315


Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
    320             325             330


Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
335             340             345             350
```

34

```
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
            355             360             365

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Gln Tyr
            370             375             380

Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Pro Asp Asp
            385             390             395

Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn Leu
    400             405             410

Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp
415             420             425             430

Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile Ser
            435             440             445

Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn Asn
            450             455             460

Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val Ser
            465             470             475

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
            480             485             490

Ala Ser His Leu Glu Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn
495             500             505             510

Asn Ser Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu
            515             520             525

Pro Glu Ala Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser
            530             535             540

Leu Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu
            545             550             555

Thr Leu Phe Asn Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly
    560             565             570

Ile Gln Asn Ser Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp
575             580             585             590
```

```
Val Leu Tyr Gly Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser
             595                 600             605


Tyr Leu Ser Gly Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn
             610                 615             620


Pro Ser Pro Gln Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His
             625                 630             635


Thr Gln Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr
         640                 645             650


Tyr Ala Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile
655                 660             665                 670


Val Lys Ser Ile Thr Val Ser Ala Ser
                 675
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<210>  11
<211>  1627
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Truncated human CEA with introduction of tetanus toxoid P2 and
       P30 epitopes


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<222>  (11)..(1621)

<220>
<221>  sig_peptide
<222>  (11)..(112)

<220>
<221>  mat_peptide
<222>  (113)..(1621)

<220>
<221>  misc_feature
<222>  (1253)..(1297)
<223>  Tetanus toxoid P2 epitope

<220>
<221>  sig_peptide
<222>  (1547)..(1609)
<223>  Tetanus toxoid P30 epitope

<400>  11
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gctagccacc atg gaa agt ccc tca gcc cca ccc cac cgc tgg tgt att          49
           Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile
               -30                     -25

cct tgg cag cgc ctg ctc ctg aca gca agc ctg ctg acc ttt tgg aat        97
Pro Trp Gln Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn
    -20             -15                 -10

cca ccc acg aca gcc aaa ctg act atc gag tct act cct ttc aac gtg       145
Pro Pro Thr Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val
-5               -1  1               5                   10

gcg gaa ggg aag gag gtt ctg ctc ctg gtc cat aat ctg cca cag cac       193
Ala Glu Gly Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His
            15              20                  25

ctg ttt ggt tat tca tgg tac aaa ggc gaa cgc gtg gat gga aac cgg       241
Leu Phe Gly Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg
        30              35                  40

caa att atc ggg tat gtt atc ggc aca cag cag gcc aca ccc ggt ccg       289
Gln Ile Ile Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro
    45                  50                  55

gct tac agt ggg cgc gaa att atc tat cca aat gcc agc ctg ctg atc       337
Ala Tyr Ser Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile
60                  65                  70                  75

caa aac att atc cag aat gac act ggc ttc tac aca ctg cat gtc atc       385
Gln Asn Ile Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile
                80                  85                  90

aaa agc gat ctg gtg aac gag gaa gca acg ggt cag ttt cgg gtt tat       433
Lys Ser Asp Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr
            95                  100                 105

ccc gaa ctg cct aag cca tca att tct tcc aat aac agt aaa ccc gtc       481
Pro Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val
            110                 115                 120

gaa gac aaa gac gcc gtg gct ttc acg tgc gag cct gaa aca caa gat       529
Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp
        125                 130                 135

gca act tac ctg tgg tgg gtt aac aat cag agc ctg cca gtc tca ccc       577
Ala Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro
140                 145                 150                 155

cgc ctg cag ctg agc aac gga aat cgg acc ctg aca ctc ttt aac gtg       625
Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val
                160                 165                 170

acg cgc aat gac act gcc tct tat aag tgt gag aca caa aac cct gtt       673
Thr Arg Asn Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val
                175                 180                 185

tca gcg cgg cgc agc gat agt gtt atc ctg aat gtg ctg tac ggc cca       721
Ser Ala Arg Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro
        190                 195                 200
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gac gct ccc acc att tcc ccg ctg aac act tct tat cgc tca ggg gaa        769
Asp Ala Pro Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu
    205             210             215

aat ctg aac ctg agc tgc cac gcc gca agc aat cca ccc gcg cag tac        817
Asn Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr
220             225             230             235

agt tgg ttc gtc aac ggt aca ttt cag caa tct act cag gaa ctg ttc        865
Ser Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe
            240             245             250

atc cct aat att acg gtt aac aat tca ggc agc tat aca tgt cag gct        913
Ile Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala
        255             260             265

cat aac tcc gac aca ggg ctg aat cgg act aca gtg acg acg atc aca        961
His Asn Ser Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr
        270             275             280

gtc tac gcc gag cca ccc aaa ccc ttt att act tct aac aat agt aac       1009
Val Tyr Ala Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn
    285             290             295

cca gtt gaa gat gag gac gca gtg gct ctg acc tgc gaa cct gag atc       1057
Pro Val Glu Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile
300             305             310             315

caa aat aca acc tat ctg tgg tgg gtc aac aat cag tca ctg cca gtt       1105
Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val
            320             325             330

agc ccc cgc ctg cag ctc agc aac gac aat cgg act ctg acg ctg ctc       1153
Ser Pro Arg Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu
            335             340             345

tct gtg aca cgc aac gat gtc ggt cca tac gaa tgt ggc att caa aat       1201
Ser Val Thr Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn
        350             355             360

gaa ctg tca gtt gac cac agt gat ccc gtg atc ctg aac gtc ctg tat       1249
Glu Leu Ser Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr
    365             370             375

gga cag tac atc aaa gct aac tcc aaa ttc atc ggc atc acc gaa ctg       1297
Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
380             385             390             395

cca gac gac cct acc att agc cca tcc tac act tat tac cgg ccc ggg       1345
Pro Asp Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly
            400             405             410

gtt aat ctg tct ctg agc tgc cat gcc gcg tca aac cca ccc gca cag       1393
Val Asn Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln
            415             420             425
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tac agc tgg ctg atc gat ggc aat att cag caa cac aca cag gag ctg      1441
Tyr Ser Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu
        430              435              440

ttc atc agt aac att aca gaa aaa aat tct gga ctg tat acg tgt cag      1489
Phe Ile Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln
        445              450              455

gct aac aat tcc gcc agc ggt cat agc cgc aca act gtg aag acg atc      1537
Ala Asn Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile
460              465              470              475

act gtc tct ttc aac aac ttc acc gtt tcc ttc tgg ctg cgc gtt cca      1585
Thr Val Ser Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
                480              485              490

aaa gtt tcc gct tcc cac ctg gaa ggt acg tca ccc taatga             1627
Lys Val Ser Ala Ser His Leu Glu Gly Thr Ser Pro
                495              500
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<210>  12
<211>  537
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Truncated human CEA with introduction of tetanus toxoid P2 and
       P30 epitopes

<400>  12
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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
            -30              -25              -20


Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
        -15              -10               -5


Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
    -1  1          5              10


Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
15              20              25              30


Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
            35              40              45


Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
            50              55              60


Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
        65              70              75
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Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
    80   85   90

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
95   100   105   110

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
            115   120   125

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
            130   135   140

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
        145   150   155

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
    160   165   170

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
175   180   185   190

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
            195   200   205

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
            210   215   220

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
        225   230   235

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
    240   245   250

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
255   260   265   270

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
            275   280   285

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
            290   295   300

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
        305   310   315

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
    320   325   330

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
335   340   345   350

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
            355   360   365

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Gln Tyr
            370   375   380

Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Pro Asp Asp
        385   390   395

Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn Leu
    400   405   410

Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp
415   420   425   430

Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile Ser
            435   440   445

Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn Asn
            450   455   460

Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val Ser
        465   470   475

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
    480   485   490

Ala Ser His Leu Glu Gly Thr Ser Pro
495   500

<210> 13
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 13

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1   5   10   15

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<210>  14
<211>  21
<212>  PRT
<213>  Clostridium tetani

<400>  14

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1               5                   10                  15


Ala Ser His Leu Glu
            20


<210>  15
<211>  13
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Artificial universal MHC Class II DR binding sequence

<400>  15

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1               5                   10
```

(54) Title: IMMUNOGENIC CARCINOEMBRYONIC ANTIGEN (CEA)

(57) Abstract: The present invention provides for methods for immunizing actively against autologous carcinoembryonic antigen (CEA). The method encompasses that the immune system is engaged with variant CEA which is either administered as a protein vaccine, or is effected expressed by nucleic acid vaccination or live/viral vaccination. Preferred embodiments include immunization with variants that include at least one foreign T-helper epitope introduced in the CEA sequence. The T helper epitope may for example be a tetanus toxoid epitope, such as the P2 and P30 epitopes. Also disclosed is variant proteins, DNA, vectors, and host cells useful for practicing the method of the invention.

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7   A61K39/00   C07K14/715   A61P35/00   C12N15/11   //A61K39/08

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7   A61K   C07K   C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, MEDLINE, WPI Data, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 00 20027 A (M & E BIOTECH A S ;NIELSEN KLAUS GREGORIUS (DK); BIRK PETER (DK);) 13 April 2000 (2000-04-13) cited in the application claims 1-9,18-36,45-47,54,62,65 --- -/--	1-57

[X] Further documents are listed in the continuation of box C.   [X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
1 August 2003	18 AUGUST 2003

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	IDA CHRISTENSEN / ELY

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	NAIR S K ET AL: "Induction of carcinoembryonic antigen (CEA)-specific cytotoxic T-lymphocyte responses in vitro using autologous dendritic cells loaded with CEA peptide or CEA RNA in patients with metastatic malignancies expressing CEA." INTERNATIONAL JOURNAL OF CANCER. JOURNAL INTERNATIONAL DU CANCER. UNITED STATES 2 JUL 1999, vol. 82, no. 1, 2 July 1999 (1999-07-02), pages 121-124, XP002249873 ISSN: 0020-7136 cited in the application the whole document ---	1-57
Y	WO 01 49317 A (AVENTIS PASTEUR LTD ;BARBER BRIAN H (CA); EMTAGE PETER (CA); SIA C) 12 July 2001 (2001-07-12) claims ---	1-57
A	WO 99 19478 A (BARZAGA ELENE ;US HEALTH (US); ZAREMBA SAM (US); SCHLOM JEFFREY (U) 22 April 1999 (1999-04-22) the whole document -----	1-57

INTERNATIONAL SEARCH REPORT

PCT/DK 03/00031

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.: 1-40, 55
   because they relate to subject matter not required to be searched by this Authority, namely:

   see FURTHER INFORMATION sheet PCT/ISA/210

2. [X] Claims Nos.: 41-43, 48 (partially)
   because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

   see FURTHER INFORMATION sheet PCT/ISA/210

3. [ ] Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest
[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1998)

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

Continuation of Box I.1

Claims Nos.: 1-40, 55

Claims 1-40 and 55 relate to methods of treatment of the human or animal body by surgery or by therapy or diagnostic methods practised on the human or animal body (Rule 39.1(iv)). Nevertheless, a search has been executed for these claims. The search has been based on the alleged effects of the compounds or compositions.

Continuation of Box I.2

Claims Nos.: 41-43, 48 (partially)

Present claims 41-43 and 48 relate to an extremely large number of possible polypeptides and nucleic acid fragments. Support within the meaning of Article 6 PCT and disclosure within the meaning of Article 5 PCT is to be found, however, for only a very small proportion of the polypeptides and nucleic acid fragments claimed. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Consequently, the search has been carried out for those parts of the claims which appear to be supported and disclosed, namely those parts related to the polypeptides and nucleic acid fragments of SEQ ID Nos. 5-12. Further, the search has covered the general aspects of the invention to some extent.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 0020027	A	13-04-2000	AU	751709 B2	22-08-2002
			AU	5851099 A	26-04-2000
			CA	2345817 A1	13-04-2000
			CN	1323217 T	21-11-2001
			CZ	20011049 A3	14-08-2002
			WO	0020027 A2	13-04-2000
			EE	200100203 A	15-10-2002
			EP	1117421 A2	25-07-2001
			HR	20010319 A1	30-06-2002
			HU	0103976 A2	28-02-2002
			JP	2002526419 T	20-08-2002
			NO	20011586 A	31-05-2001
			PL	347977 A1	06-05-2002
			TR	200100936 T2	21-08-2001
WO 0149317	A	12-07-2001	AU	2658801 A	16-07-2001
			WO	0149317 A2	12-07-2001
			CA	2394597 A1	12-07-2001
			EP	1246646 A2	09-10-2002
			JP	2003519197 T	17-06-2003
WO 9919478	A	22-04-1999	AU	745863 B2	11-04-2002
			AU	9500498 A	03-05-1999
			CA	2308127 A1	22-04-1999
			EP	1017810 A1	12-07-2000
			JP	2002500002 T	08-01-2002
			WO	9919478 A1	22-04-1999